

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 18:07:37 ; Search time 4046 Seconds
(without alignments)
16047.421 Million cell updates/sec

Title: US-09-914-098-55
Perfect score: 1498
Sequence: 1 gcacgaggtccgttgcgtg.....aaaaaaaaaaaaaaaaact 1498

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sv.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.on.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
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28: em.un.*
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41: em.htgo.other.*

SUMMARIES

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1	706.8	47.2	1396	8	AF213937	Prunus du
2	672.8	44.9	1702	6	BD224793	BD224793 Novel pla
3	652.8	43.6	1170	6	BD224663	BD224663 Novel pla
4	652.8	43.6	1615	8	BNLPAAT	Z95637 B.napus mRN
5	651.4	43.5	1480	8	AY084461	AY084461 Arabidops
6	642.2	42.9	1515	6	AS2744	AS2744 Sequence 3
7	642.2	42.9	1515	6	AS2744	AS2744 Sequence 3
8	640.6	42.8	1486	8	LDAGPATMR	AR349252 Sequence
9	548.8	36.6	1514	6	A38840	Z48730 L.douglasii
10	548.8	36.6	1514	6	AR062686	AR062686 Sequence 1
11	548.8	36.6	1514	6	AR135355	AR135355 Sequence
12	548.8	36.6	1518	8	ZM1AG3PAT	Z29518 Z.mays (Bla
13	525	35.0	1415	8	BT009239	BT009239 Triticum
14	458	30.6	1367	8	BNAGPATRF	Z49860 B.napus mRN
15	33.1	22.1	714	8	AF479037	AF479037 Triticum
16	190.6	12.7	312	6	BD224753	BD224753 Novel pla
17	150	10.0	279	6	BD224754	BD224754 Novel pla
18	149.2	10.0	11446	8	AC143341	AC143341 Medicago
19	145	9.7	304	6	BD224755	BD224755 Novel pla
20	132	8.8	259	6	BD224756	BD224756 Novel pla
21	129.4	8.6	235	6	BD224757	BD224757 Novel pla
22	126.4	8.4	3509	5	BC043776	BC043776 Xenopus l
23	121.8	8.1	1577	9	BC011971	BC011971 Homo sapi
24	121.8	8.1	1660	6	BD265488	BD265488 Mammalian
25	121.8	8.1	1660	6	AR370494	AR370494 Sequence
26	121.8	8.1	1660	6	AF156774	AF156774 Homo sapi
27	120.2	8.0	1128	6	AX239832	AX239832 Sequence
28	120.2	8.0	1333	9	E39269	E39269 Gene encodi
29	120.2	8.0	1333	9	AB040138	AB040138 Homo sapi
30	120.2	8.0	1769	6	AR339350	AR339350 Sequence
31	120.2	8.0	1832	6	AX239824	AX239824 Sequence
32	120.2	8.0	1960	6	AX317982	AX317982 Sequence
33	120.2	8.0	2377	9	BC063552	BC063552 Homo sapi
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35	120.2	8.0	3060	6	AX376270	AX376270 Sequence
36	120.2	8.0	3060	6	AX697228	AX697228 Sequence
37	120.2	8.0	3060	9	AY358704	AY358704 Homo sapi
38	118.4	7.9	265	6	BD224724	BD224724 Novel pla
39	118.4	7.9	265	6	BD224725	BD224725 Novel pla
40	114.4	7.6	1153	10	AY167588	AY167588 Mus muscu
41	113.8	7.6	1868	10	AB067572	AB067572 Rattus no
42	112.8	7.5	3378	10	BC058519	BC058519 Mus muscu
43	112.8	7.5	3379	10	BC052382	BC052382 Mus muscu
44	110.4	7.4	3955	9	AK125804	AK125804 Homo sapi
45	108.6	7.2	1523	6	BD265489	BD265489 Mammalian

ALIGNMENTS

RESULT 1	AF213937	1396 bp	mRNA	linear	PLN 26-DEC-1999
LOCUS	Prunus dulcis	1-acyl-sn-glycerol-3-phosphate acyltransferase mRNA,			
DEFINITION	complete cds.				
ACCESSION	AF213937				
VERSION	AF213937.1	GI:6635839			
KEYWORDS					
SOURCE	Prunus dulcis (almond)				
ORGANISM	Prunus dulcis				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.				
REFERENCE	1 (bases 1 to 1396)				
AUTHORS	Campalans,A., Pages,M. and Messeguier,R.				

Pred. No. is the number of results predicted by chance to have a

TITLE Identification of differentially expressed genes during dehydration
in almond (*Prunus amygdalus*) using the cDNA-AFLP technique
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1396)
AUTHORS Campalans, A., Pages, M. and Messeguer, R.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-1999) Genetica Molecular, Centre d'Investigacio i
Desenvolupament (CSIC), C/ Jordi Girona, 18-26, Barcelona 08034,
Spain

FEATURES

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/note="similar to LPA-A7"

CDS

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RAQEAATAGLPVPRNVLPRTKGFVTAVSQMRSPAPALYDVTVAIKSPSPAPTMRL
FGRSVVHVHKKHVMKDLPEDEAVQWCKDI FVAKDALLDHTVEQTFGDQKLV
TGRPKSLVVTWACLILGALFLYMSLLSWKGI AFSA LGLGVTVVLMQLIRF
QSERSTPAPVAPTNNKNKGSSGKPEKQ"

ORIGIN

Query Match 47.2%; Score 706.8; DB 8; Length 1396;

Best Local Similarity 80.4%; Pred. No. 3.7e-164;

Matches 864; Conservative 0; Mismatches 207; Indels 3; Gaps 3;

QY 181 CCGGCTCTTGTATATCATTCATTCAGGCAATATGC-TATGTGCTGCTGAAGCCCGGTGTCG 239
DB 1 CCAGCCCTCGTGTCTATCTCTCATTCAGGCGATTGCTTCATCTTATTCGGCCCTGTGCT 60
QY 240 AAAAGTGTGTACAGAGGATCAACCGGTAGTAGCAGAGCTCTTGCGCTGGAGCTGTGA 299
DB 61 AAGAAATTATCCAGAAGGATAACAGAGTGGT-CCAGAATTATTGTGGCTGAAGCTGGTG 119
QY 300 TGGCTTATTGATTGTGGCGGAGGAGTTAAGGTCCAAATATTACAGATCATGAACCTTT 359
DB 120 TGGCTCATTGATTGTGGCGAGGTGTTAAGATTCAAGTTTACAGACCAATGAACCTTT 179
QY 360 CGTTAATGGGTAAGAGCATGCCTGTGTATAGCAATACACAGAAGTGATTTGATTGG 419
DB 180 -ATTAAATGGGTAAGAACATGCCTTGTATATCCCAATCATAGAAGTGATTTGATTGG 238
QY 420 CTGTGTGATCGGTTTTCAGCTCAGCTTTCAGGTTGCTTTCGAGCACTCTAGCTGTGATG 479
DB 239 CTGTGTGATCGGTTTTCAGCTCAGCTTTCAGGTTGCTTTCGAGCACTCTAGCTGTGATG 298
QY 480 AAGAAATCTTCAAGTTTCTCCGGTCAATGGCTGGTCAATGGTTTCTGAGTATCTT 539
DB 299 AAGAAATCATCAAAATTCCTTCGGTCAATGGTGGTCAATGGTTTCTGAGTATCTT 358
QY 540 TTCTCGAGAGAGCTTGGCCCAAGGATGAAGACATTAAGTCAAGGATCCAGGCACTG 599
DB 359 TTCTTGAAGAGAGCTGGCCCAAGGATGAAGACATTAAGTCAAGGATCCAGGCACTG 418
QY 600 AGTCATTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGAACGCGCTTTTACACAG 659
DB 419 AAGGACTTCCCTCAGCCCTTTTGGTGGCTCTGTTGTAGAAGCACTCGTTTACACAG 478
QY 660 GCCAAATATAGCTGTCTAGGAATATGCCACTTCCACTGGATGCTGTTCCTAGAAAT 719
DB 479 GCAAAGCTTTTAGCAGCTCAAGAAATATGACCGCCGCAACAGGCGCTTCTCTCCCTAGAAAT 538
QY 720 GTTTTGAATCCAAAGAACTAAGGGTTTGTGTTCTGCAGTAGTCAATGCTGCTCATTTGTT 779
DB 539 GTTTTGAATCCCAAGGTTTGTGTTCTGCAGTAGTCAATGCTGCTCATTTGTT 598
QY 780 CCGGCTCTTGTATATCATTCATTCAGGCAATATGC-TATGTGCTGCTGAAGCCCGGTGTCG 239

DB 599 CCAGCCATTTATGATTAACAGTGGCTATTTCCTAAAAAGTTCACCTGCACCGCAATGCTA 658
QY 840 AGACTCTTCAAGGACAAACCTTCAGTGGTGCATGTTTCATATCAAGAGGATTTGATGAAG 899
DB 659 AGACTCTTCAAGGACAAACCTTCTGGTGCATGTCACATCAAGAGGATTTGATGAAG 718
QY 900 GAATGCCAGATACAGATGAGGCTGTGTCTCAATGGTGTGCGAGATATATTTGTGGCCAA 959
DB 719 GATTTCCTGAAACTGATGAGGCTGTGCACAAATGGTGTAAAGATATATTTGTAGCCAAG 778
QY 960 GATGCTTTGTAGACAAACATATGGCTGAGGCTACTTTAGTATCAAGAGCTGCAGGAT 1019
DB 779 GATGCTTTGTAGACAAACATATGGCTGAGGCTACTTTAGTATCAAGAGCTGCAGGAT 838
QY 1020 ACTGGTCGACCAATAAAGTCTCTTCTGGTAGTATATCTTGGGCGGTGCTGCTGTTGTGG 1079
DB 839 ACTGGTCGCGCGCTAAAGTCTCTTTTGGTGTTCAGAGCTTGGGCTGTTACTTATTG 898
QY 1080 GGGTCTGTAAGTTCCTGCAATGGCTTCTGTTACTCTCTTCTGGAAGGCTTTCGATTT 1139
DB 899 GGGGCTCTAAAGTTCCTCTACTGGTCTTCGCTTCTATCCTCGTGAAGGCTTATGCA 958
QY 1140 TCAGCTTTTGGTGTGGCAGTGTGTTACTGCACATTATGCAAAATTCGATTCATTCACAG 1199
DB 959 TCAGCATTTGGTGTGGGCGTGTGTTACTGCTCTTATGCAGATCTTGTATTCGATTTGCG 1018
QY 1200 TCAGAGCTTCAAAACCCGCGCCAGATCGTGGCTGCAAAAGTCAAAAACAAAGGG 1253
DB 1019 TCAGAGCGTTCACACACCTGCCCGAGTGGCTCTTACAAATAACAAAACAAAGGG 1072

RESULT 2

BD224793

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS

PN

PD

PF

PR

PI

PC

FH

FT

FEATURES

source

ORIGIN

Query Match

Best Local

Matches

Conservative

Mismatches

Indels

Gaps

Length

Pred. No.

Indels

Gaps

Length

Pred. No.

Indels

Gaps

Length

Db 137 GGCTAATCTTTGAATTTGTTGGTGAAGCCATGGGGATCCAGCTGGGCTGTGATTGTACC 196
QY 158 ATTGGGCGCTCTCTTCTCGCTCCGCTCCCTTGTGTTAATCTCATTCAGGCAATATGCTA 217
Db 197 GCTTGGCTTCTCTTCT 256
QY 218 TGTCTGTCTAAGCCCGTGTGCAAAAGTTTGTACAGAGGATCAACCGGCTAGTAGCAGA 277
Db 257 TGTCTGTCTGCGCCACTGTCAAGNNATCATACAGAGGATTAACAGGCTGCTGTGGA 316
QY 278 GCTCTGTGCTGAGGCTGTATGCTTATGTTGTTGGGCAAGATTAAAGTCCCAAT 337
Db 317 ATTGTTGTGCTGAGCTGTATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 376
QY 338 ATTCACAGATCATGAACCTTTGTTTAAATGGGTAAGAGCATGCACTTTGTGATAAGCAA 397
Db 377 GTTCACAGATCTGATACCTTTCCGCTAAAGGTAAGAGCATGCACTTTGTGATACAA 436
QY 398 TCACAGAGTATATGATGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 457
Db 437 CCACAGAGTATATGATGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 496
QY 458 TGGCAGCATCTAGCTGTGATGAAGAAATCTTCAAGTTTCTGCGGCTCATTCGGCTGGTC 517
Db 497 GGGAGACACTGCTGTCTGATGAAGAAATCATCANAGTTTCTCCGCTCATAGTTGGTC 556
QY 518 AATCTGCTTTCTGAGTATCTTTCTGAGAGAGAGTTGGGCAAGATGAAGACATTT 577
Db 557 TATCTGCTTTCTGAGTACCTTTCTTGTGAGAGAGCTGGGCAAGATGAAGACATTT 616
QY 578 AAGCTCAGGATCCAGGCTGAGTGTATCCCTCTTCCCTTTTGGCTAGCTCTCTTGT 637
Db 617 GAAGTTAGGCTTTCAAGCCCTCAAGGACTACCTCTGCTCTTCTGCTGTGCTCTTCT 676
QY 638 AGAAGGAACGGCTTTTACAGAGGCAAACTATTAGCTGCTCAGGAATATCCACTCCAC 697
Db 677 AGAAGGAACAGATTTTACCAGCTAACTTTTAGCAGCTCAAGATATGCTACTTCAAT 736
QY 698 TGGATTGCTGCTTCTAGAAATGTTTGTATCCAGAACTAAAGGTTTCTGCTGCTGCT 757
Db 737 GGGATTGCTGCTTCTAGAAATGTTTGTATCCCTCTGCTGCTGCTGCTGCTGCTGCT 796
QY 758 AAGTCATATGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 817
Db 797 GAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 856
QY 818 TTCCCTGCTCTCAATGCTAAGCTCTTCAAGGGAACACTTCAAGTGGTGTGATGTCA 877
Db 857 TTCTTCGAGGCTACATGCTCAGACTTTTCAAGGCGGAGCATCCAGGTTCTATGTACA 916
QY 878 TATCAGAGGCTATGTAGAGGAGCTGCCAGATACAGATGAGCTGTTGCTCAATGGTG 937
Db 917 CATCAAGCGGCTCGATGAAGATCTCCCTGAAGCAGCAGATGATGTGCAATGGTG 976
QY 938 TCGAGATATTTGTGGCCAAAGGATGCTTTGTAGACAAACATATGCTGAGGCTACTTT 997
Db 977 TCGAGACACATTCGTCGCAAGGATGCTCTCTGCAAGCATAATGTAGATGACACTTT 1036
QY 998 TAGTGATCAAGAGCTGAGGATGCTGCTGAGCAATAGCTCTTCTGCTAGTATATC 1057
Db 1037 CGAGATGAGTATCTGCAAGGACTGCGCGGCTTTGAAATCTCTCTTTGTAGCAGTCT 1096
QY 1058 TTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1117
Db 1097 TTGGGCTATGCTCTATCTCTCTGAGGTTTGAATTCCTACAGTGTGCTCTCTCTATC 1156
QY 1118 TTCCTGGAAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1177
Db 1157 ATCATGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1216
QY 1178 AATTCGATCAATCTCAGCTGAGGCTTCAAAACCGGCGAGATCGCTGCTGCAAA 1237
Db 1217 GATCTTAATCCAAATTTCTCAATCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1276

QY 1238 GTCAAAAACAAAGGGTC 1255
Db 1277 GCCCAAGAACATGGTATC 1294

RESULT 3

BD224663

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Novel plant acyltransferases.
BD224663
BD224663.1 GI:33034433
JP 2002525105-A/12.
Arabidopsis sp.
Arabidopsis sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1170)
Lassner, M.W., Emig, R.A., Ruzinsky, D.M. and Eenennaam, A.V.
Novel plant acyltransferases
Patent: JP 2002525105-A 12 13-AUG-2002;
CALGENE LLC
OS Arabidopsis sp.
PN JP 2002525105-A/12
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572337
PR 25-SEP-1998 US 60/101939
PI MICHAEL W LASSNER, ROBIN A EMIG, DIANE M RUZINSKY, ALISON VAN
PI EENENNAAM
PC C12N15/09, A01H5/00, C12N5/10//C12N9/10, C12N15/00, C12N5/00 CC
Novel plant acyltransferases
PH Key Location/Qualifiers
FT source 1..1170
/organism='Arabidopsis sp.'

FEATURES

source

1..1170

/organism='Arabidopsis sp.'

/mol_type='genomic DNA'

/db_xref='taxon:29726'

ORIGIN

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Best Local Similarity 74.2%; Pred. No. 8,9e-151;
Matches 825; Conservative 0; Mismatches 287; Indels 0; Gaps 0;
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Db 10 GCTGAGCTGTATCGTGGCTTTGGGCTCTCTCTTCATATCTGCTCTCGCTGTCAT 69
QY 198 CTCATTACGCAATATGCTATGTCGCTAAGCGCGGTGTCGAAAGTTTGTACGAAGG 257
Db 70 CTCTTTACGCGAGTTTGTCTATGTACTCATTCGACCACTGTCTAAGAACACATACAGAAA 129
QY 258 ATCAACCGGCTAGTAGCAGGCTCTGCTGGCTGGAGCTGTATGGCTTATGATTGCTGG 317
Db 130 ATTAAACCGGCTGGTTCGCAAAACCTTGTGGTGGAGCTGTATGGATAGTGTGCTGG 189
QY 318 GCAGGAGTTAAGGTCCAAATATTACAGATCATGAACCTTTCTGTTAATGGGTAAAGAG 377
Db 190 GCTGGAGTTAAGATCCAGTTTGTGATATGAGACCTTCAATCGAATGGCAAGAA 249
QY 378 CATGCACTGTGATAGCAATACAGAGTGATTTGATGGCTTGTGGATGGGTTTCA 437
Db 250 CATGCTCTTGTCTTTGTAATCAACGAAGTATGATTTGGCTTGTGGATGGATTCTG 309
QY 438 GCTCAGGTTACAGTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAAGTT 497
Db 310 GCTCAGGCTCAGTTGCTTGGGAAGGCAATAGCTGTATGAAGAGCTTCCAAATTC 369
QY 498 CTCGCGCTCATTCGCTGGTCAATGTGTTTCTGAGTATCTTTTCTGAGAGAAAGTTGG 557
Db 370 CTTCCAGTCATAGGCTGGTCAATGTGTTTCTCGAGTATCTCTTCTGGAAGAAATTTG 429

QY 678 CAGGAATATCCACTTCCACTGATTCCTGTTTCCCTAGAAATGTTTGTATTCAGAACT 737
 Db 701 CAAGAGTACGACGCTCCTCTGAGTTGCTGTCCTTCGAAATGTTGTTGTTCTCGCAC 760
 QY 738 AAGGTTTCTTCTCAGTAAGTCATATGCGCTCATTTGTTCTCTGCCATTTATGATGA 797
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 QY 798 ACAGTAGCCATCCCTAAGAGTTCCCTGCTCTTACAAATGCTAAGACTCTTCAAGGACAA 857
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 QY 918 GAGGCTCTTCTCAATGCTGCGATATATTTGTTGGCCCAAGGATGTTTGTAGACAA 977
 Db 941 GAGGAATTCACAGTGTGTCAGAGATCACTTTGTTGGCTAAGGATGCTGTTTACACAA 1000
 QY 978 CATATGCTGAGGTACTTTTAGTATCAAGAGCTGCGAGATGCTGCTGACCAATAAG 1037
 Db 1001 CACATAGCTGACAGACTTTTCCCGGTTCAGAAAGACAGAACTTGGCGCTCCATAAG 1060
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RESULT 5
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 DEFINITION Arabidopsis thaliana clone 108727 mRNA, complete sequence.
 ACCESSION AY084461
 VERSION AY084461.1 GI:21403171
 KEYWORDS FLI_CDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 1480)
 Haas, B.J., Volkov, N., Town, C.D., Troughan, M., Alexandrov, N.,
 Feldmann, K.A., Flavell, R.B., White, O., and Salzberg, S.L.
 Full-length messenger RNA sequences greatly improve genome
 annotation
 Genome Biol. 3 (6), RESEARCH0029 (2002)
 22088475
 12093376
 2 (bases 1 to 1480)
 Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
 Feldmann, K.
 Full-length cDNA from Arabidopsis thaliana
 Unpublished
 3 (bases 1 to 1480)
 Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
 Feldmann, K.
 Direct Submission
 Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
 Malibu, CA 90265, USA
 This clone sequence is one of 5,000 Ceres full-length cDNAs made

available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES

Location/Qualifiers

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 ITISALGLGIITLCMIQLIRSQSERSTPAKVPAKPDNHPHSPSSQTEKEK"

CDS

ORIGIN

Query Match 43.5%; Score 651.4; DB 8; Length 1480;
 Best Local Similarity 74.1%; Pred. No. 2e-150;
 Matches 824; Conservative 0; Mismatches 288; Indels 0; Gaps 0;
 QY 138 GCAGGGCGGTGGTGATGACATTTGGCGCTCTTCTTCGCTCGCGCTCTCTTTAA 197
 Db 247 GCTGAGCTGTCTATGCTGCTTTGGGCTTCTTCTTCATATCTGCTCGCTGCAAT 306
 QY 198 CTCATTACGCAATATGCTATGCTGCTGAAGCGGTGTCGAAAGTTTGTACAGAAG 257
 Db 307 CTCTTTACGACAGTTGCTATGCTATCTATTCGACCACTGTCTAAGAACACATACAGAAA 366
 QY 258 ATCAACCGGTAGTACAGAGCTCTTGTGCTGGAGCTTGTATGGCTTATTGATGGTGG 317
 Db 367 ATTAACCGGTGGTTCAGAAACCTTGTGTTGGAGCTTGTATGATGATGATGCTGG 426
 QY 318 GCAGGAGTTAAGTCCAAATATTCAAGATCATGAACCTTTCTGTTTAAATGGGTAAGAG 377
 Db 427 GCTGGAGTTAAGATCCAAGTGTCTGATATAGACCTTCAATCGAATGGCAAGAA 486
 QY 378 CATGCACTTGTGATAGCAATCAAGAGTATGATGCTTGTGCTGGAGTTTCA 437
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LOCUS AR349252 1515 bp mRNA linear PAT 17-AUG-2003
DEFINITION Sequence 3 from patent US 6583340.
ACCESSION AR349252
VERSION AR349252.1 GI:33749968
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1515)
AUTHORS Slabas,A.R., Brown,A.P., Brough,C.L. and Kroon,J.T.M.
TITLE DNA sequence encoding plant 2-acyltransferase
JOURNAL Patent: US 6583340-A 3 24-JUN-2003;
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Matches 821; Conservative 0; Mismatches 298; Indels 0; Gaps 0;

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Qy 1186 TTCAATTTCTCAGCTCAGAGCGTTTCAAAACCGGCCAAGA 1224
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LDGAPATMR 1486 bp mRNA linear PLN 17-NOV-1995
L.douglasii mRNA for 1-acyl-sn-glycerol-3-phosphate acyltransferase
(purative).
ACCESSION Z48730
VERSION Z48730.1 GI:1067137
KEYWORDS 1-acyl-sn-glycerol-3-phosphate acyltransferase.
SOURCE Limnanthes douglasii (Douglas's meadowfoam)
ORGANISM Limnanthes douglasii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Limnathaceae; Limnanthes.
REFERENCE 1 (bases 1 to 1486)
AUTHORS Brown,A.P., Brough,C.L., Kroon,J.T. and Slabas,A.R.
TITLE Identification of a cDNA that encodes a
1-acyl-sn-glycerol-3-phosphate acyltransferase from Limnanthes
douglasii
JOURNAL Plant Mol. Biol. 29 (2), 267-278 (1995)
MEDLINE 96046746
PUBMED 7579178
REFERENCE 2 (bases 1 to 1486)
AUTHORS Brown,A.P., Brough,C.L., Kroon,J.T. and Slabas,A.R.
TITLE Identification of a cDNA that encodes a
1-acyl-sn-glycerol-3-phosphate acyltransferase from Limnanthes
douglasii
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1486)
AUTHORS Brough,C.L.
TITLE Direct Submission
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Db 1065 GTGCTCTGCTGTTTGGCGCATCGAGTTCTTCAAGTGGACACAGCTTCTGTGCGAGTG 1124

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LOCUS AR062686 Sequence 1 from patent US 5843739.
DEFINITION AR062686
ACCESSION AR062686
VERSION AR062686.1 GI:5990377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1514)
AUTHORS Slabas, A. Ryszard, and Brown, A. Paul.
TITLE DNA encoding 2-acyltransferases
JOURNAL Patent: US 5843739-A 1 01-DEC-1998;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 36.6%; Score 548.8; DB 6; Length 1514;
Best Local Similarity 68.8%; Pred. No. 5.5e-125;
Matches 770; Conservative 0; Mismatches 347; Indels 3; Gaps 1;

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Qy 164 CTTGCTCTTCTTGGCTCCGCGCTCTTGTAAATCTCATTCAGGCAATATGCTATGCTG 223

Db 168 CTTGCTCTTCTTGGCTCCGCGCTCTTGTAAATCTCATTCAGGCAATATGCTATGCTG 227

Qy 224 CTTAGGCGCGGTGTCGAAAGTTTGTACAGAGGATCAACCGGTAGTAGAGAGCTCTT 283

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ORIGIN

Query Match 36.6%; Score 548.8; DB 6; Length 1514;
Best Local Similarity 68.8%; Pred. No. 5.5e-125;
Matches 770; Conservative 0; Mismatches 347; Indels 3; Gaps 1;

Qy 104 GCTGGCTGGGCTGGCGTATGCGCATGCTATTGCGACAGCGCGGTGGTGGTACCATTTGGG 163

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Q	y	824	TGCTCTTACAATGCTTAAGACTCTTCAAGGGACAACCTTTCAGTGGTGCATGTTTCATATCAA	883
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Q	y	1004	TCAAGAGCTGCAGGATACTGTCACCAATAAAGATCTCTTCTGGTAGTTATATCTTGGGC	1063
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Q	y	1064	GTGCTGTTGTTGCGGGGCTGTAAAGTTCCTCAATGGTCTTCGTTACTCTCTCTCTG	1123
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AUTHORS				
Plabas,A.Ryszard. and Brown,A.Paul.				
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JOURNAL				
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1518)
Brown, A.P., Coleman, J., Tomney, A.M., Watson, M.D. and Slabas, A.R.
Isolation and characterisation of a maize cDNA that complements a
1-acyl sn-glycerol-3-phosphate acyltransferase mutant of
Escherichia coli and encodes a protein which has similarities to
other acyltransferases
Plant Mol. Biol. 26 (1), 211-223 (1994)
95035993
MEDLINE
PUBMED
7948871
2 (bases 1 to 1518)
Brown, A.P.
Direct Submission
Submitted (18-JAN-1994) Adrian P Brown, Biological Sciences,
University of Durham, South, Road, Durham, County Durham, DH1 3LE,
U.K

LOCATION/Qualifiers
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Query Match 36.6%; Score 548.8; DB 8; Length 1518;
Best Local Similarity 68.8%; Pred. No. 5.5e-125;
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164 CTGCTCTCTCTGCTCGGCTCGCTCTGTTAACTCATTCAGGCAATATGCTATGTCGT 223
171 CTTGCTCTCTCTGCTCGGCTCATGCTCAAGCCATCCAGGCGCTCTCTATTTGTGAC 230
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ORIGIN

Query Match 36.6%; Score 548.8; DB 8; Length 1518;
Best Local Similarity 68.8%; Pred. No. 5.5e-125;
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164 CTGCTCTCTCTGCTCGGCTCGCTCTGTTAACTCATTCAGGCAATATGCTATGTCGT 223
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1124 GAAGGCTGTGCAATTTTTCAGCTTTTGGCTTTGTCAGTTGTTTACTGACATATGCAATTTCT 1183
1128 GAGGCTGTGCGGTTTCACTGCGCAGGATGCGGCTTGTGACGGGTGTCATGCTGCTT 1187
1184 GATTCAATTTCTCAGTCAAGCGGTTCAAACCCGCGCAAG 1223
1188 CATCATGTTTCTCCAGGCTGAGCGGTGAGCTCAGCCAGG 1227

BT009239 1415 bp mRNA linear PLN 20-JUN-2003
Triticum aestivum clone wkl.p0004.e7:fis, full insert mRNA
sequence.
BT009239
BT009239.1 GI:32128790
FLI CDNA.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 1415)
Tingey, S.V., Wolters, P., Powell, W., Dolan, M., Miao, G.-H.,
Caraher, N.R., Hanafey, M.K. and Hanney, C.F.

RESULT 13
BT009239
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

TITLE Direct Submission
JOURNAL Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

FEATURES
source Location/Qualifiers
1..1415
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Best Local Similarity 67.7%; Pred. No. 4.3e-119;
Matches 751; Conservative 0; Mismatches 355; Indels 3; Gaps 1;

QY 114 GCTGGCTGGCGATGGCTATTGACAGCGCGCGCTGGTACCATTTGGCGCTGCTCTTC 173
Db 18 GCGGGCGGCGCATGGCGAATTCCTCGTCTGCTCTGCTCGCGCTCGCGCTCTCTTC 77

QY 174 TTGCGCTCGGCTCTCTTGTAACTCATTCAGCAATATGCTATGTCGTCGTAAGCGCG 233
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QY 234 GTGTGGAAGTTGTACAGAGGATCAACCGGCTAGTACAGAGCTTTGTGCTGGAG 293
Db 138 TTCTCGAAGCGAATGTACCGGCGATCAAGTATTCCTGCGCGAGTTGTTGCGCTCAG 197

QY 294 CTGTGATGCTTATGATTTGGGCGAGGATTAAGTCCAAATATTCACAGATCATGA 353
Db 198 CTGATCTGCTTGTGACTGTGGGCGAGTATTAAGTACAGGTATGCGGATCCAGAA 257

QY 354 ACCTTTGTTTAAATGGAAGAGCATGCACTTGTGATAAGCAATCACAGAAGTGATTT 413
Db 258 ACTTGGAAATCAATGGGCAAGAGCAGCGCTTCTCATATCCAAATCATCGAAGTGACAT 317

QY 414 GATTGGCTTGTGATCGGTTTACGCTCAGGTTTACGTTGCTTGGCAGCACTTAGCT 473
Db 318 GATTGGCTTGTGATCGGTTTATAGCACAGGTTTACGATGCTTGGAAAGCGCAATAGCT 377

QY 474 GTGATGAAGAAATCTTCAAGTTTCTGCCGCTCATTGGCTGGTCAATGTGTTTCTGAG 533
Db 378 ATAATGAAGAAATCTTCAAGTTTCTTCCAGTTATTTGTTGGTCCATGTGTTTGAGAA 437

QY 534 TATCTTTTTCGAGAGAGTTGGGCAAGGATGAAGCAATTAAGTACGAGCATCCAG 593
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QY 594 CGACTGAGTATTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 553
Db 498 AGGTTGAAGACTTCTCCAGATCATTTTGGCTTGGCTTCTTCTTCTTCTTCTTCTTCT 557

QY 654 ACACAGCCAAATATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCTGTTCT 713
Db 558 ACTCCAGCAAACTTTTATGAGCTCAGGAATATGCCACTTCCACTGGATTGCTGTTCT 617

QY 714 AGAAATGTTTGTATTCAGAGCACTAGGTTTGTGCTGAGTATGCTATGCTGCTCA 773
Db 618 AGGAATGCTGATTTTCAAGCAAGGATTTGATCAGCTGATGATGATGATGATGATG 677

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Db 975 CTATATGCTGCTCATAGATTTCTTACAGTGGAGCCAGCTCTTGTGACGCTGGAAGAGTG 1034

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Db 1035 ATCTCTTTTCTGCTTCTGATTTGCAATGTAACCGCGTTATGCAATGATTCATCATGTTTC 1094

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Db 1095 TCGCAGCGGAGCGCTCAAGCTCTGCGAA 1123

RESULT 14
ENAGPATRF 1367 bp mRNA linear PLN 06-JAN-1996
DEFINITION B.napus mRNA for 1-acyl-sn-glycerol-3-phosphate acyltransferase.
ACCESSION Z49860
VERSION 1
KEYWORDS 1-acyl-sn-glycerol-3-phosphate acyltransferase.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1367)
Brown, A.P., Brough, C.I., Kroon, J.T. and Slabas, A.R.
Nucleotide sequence of a cDNA for a putative 1-acyl sn-glycerol-3-phosphate acyltransferase from rape unpublished
2 (bases 1 to 1367)
Brough, C.I.
Direct Submission
Submitted (13-JUN-1995) Clare I. Brough, Biological Sciences, University of Durham, Science, Laboratories, South Road, Durham, DH1 3LE, England
Location/Qualifiers
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CDS
Query Match 30.6%; Score 458; DB 8; Length 1367;
Best Local Similarity 72.8%; Pred. No. 1.8e-102;
Matches 590; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

QY 440 TCACGCTTACGTTGCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAGTTCT 499

Db 209 TCAGAGGTCAGGTTGCCCTAGGAAGCAGGATAGCTGTGATGAAGAAGTCCTCCAAATTTCT 268
 Qy 500 GCCGTCATTGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAAAGTTGGGC 559
 Db 269 CCCAGTCATAGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAAAGTTGGGC 328
 Qy 560 CAAGGATGAAGACATTAAGTTCAGGATCCAGGACTCAGTGAATTCCTCTTCCCTT 619
 Db 329 AAAGGATGAAGACATTAAGTTCAGGATCCAGGACTCAGTGAATTCCTCTTCCCTT 388
 Qy 620 TTGGCTAGCTCTTTTGTAGAGAAAGCGGTTTACAGAGCCAAACTATAGCTGCTCA 679
 Db 389 CTGGCTAGCTCTTTTGTGGAGGAAAGCGGTTTACAGAGCCAAACTATAGCTGCTCA 448
 Qy 680 GGAATATCCCACTTCCCACTGATGCTGCTTCCCTAGAAATGTTTGTATCCCAAGAACTAA 739
 Db 449 AGAGTACGAGCCTCTCTGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 508
 Qy 740 GGGTTTGTCTGAGTGAATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
 Db 509 AGGATTTGTGTCAGCTGTAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568
 Qy 800 AGTAGCCATCCCTAAGAGTCTCCCTGCTGCTTACAAATGCTAAGACTCTTCAAGGGCAAC 859
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 Qy 980 TATGCTGAGGATCTTTTATGATCAAGAGCTGCGGATGCTGCTGCGCAATTAAGTC 1039
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 Qy 1040 TCTTCTGTGATGATATCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1099
 Db 809 TCTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 868
 Qy 1100 ATGGTCTTCTGATCTCTTCTGGAAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1159
 Db 869 CTGGTCAATCTCTTCTGCTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
 Qy 1160 TGTTACTGCTATGCAATCTGATTCATCTCAGTTCAGAGGCTTCAAGCCGGC 1219
 Db 929 CATCACTCTGTATGAGATCTGTATCCGCTCTCTCTCAGTGGAGGCTTCAACCTGC 988
 Qy 1220 CAAGATGCTGCTGCAAGTCAAAACAA 1249
 Db 989 CAAAGTCTGCTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1018
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 AF479037
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 714)
 Li, J.R., Wang, F., Li, Q.Z. and Zhang, X.S.
 Gene isolation and expression of 1-acyl-glycerol-3-phosphate
 acyltransferase
 Unpublished

2 (bases 1 to 714)
 Li, J.R., Wang, F., Li, Q.Z. and Zhang, X.S.
 Direct Submission
 Submitted (29-JAN-2002) College of Life Science, Shandong
 Agricultural University, Dai Zong Street 61, Taian, Shandong
 271018, P.R. China
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 Best Local Similarity 71.6%; Pred. No. 5e-71;
 Matches 447; Conservative 0; Mismatches 176; Indels 1; Gaps 1;
 Qy 377 GCATGCACTGTGATAGCAATCACAGAGTGTATGTTGCTGTTGATGGGTTTC 436
 Db 3 GGAGCCCTTCTAATATCCCAATCATGAGTGAATGTTGCTGTTGATGGGTTTC 62
 Qy 437 AGCTCAGCGTTTCAGTGTGTTCTGTCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTT 496
 Db 63 AGCAGCGTTTCAGTGTGTTCTGTCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTT 122
 Qy 497 TCTCCGCTCATGGCTGCTCAATGTTGTTTCTGAGTATCTTTTCTGAGAGAGCTG 556
 Db 123 CTTTCCAGTATTGTTGGTCCATGTTGTTGAGTATCTCTTTTGGAGAGAGCTG 182
 Qy 557 GGCAGAGATGAAGCAATTAAGTTCAGGCTGTCAGGCTGAGTGTATTCCTCTTCC 616
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 Qy 617 CTTTGGCTAGCTCTCTTTGAGAGAGCGGTTTACACAGGCAAACTATAGCTG 676
 Db 243 ATTTTGGCTGCTCTTTTGTGAGGTAACAAGATTACTCCAGCAAACTTTTAGCAGC 302
 Qy 677 TCAGGAATATGCCACTTCCACTGGAATGCTGTTCTCTAGAAATGTTTGTATCCAAAGAC 736
 Db 303 TCAAGATATGCAATCTCACAGGTTTGAAGGCTTAGGAATGTGCTGATTCACGAAC 362
 Qy 737 TAAGGTTTGTCTGAGTGAATGATGATGCTGCTATTTGTTCTGCTGCTATTTATGATGT 796
 Db 363 AAAGGATTTGTATCAGCTGTAAAGTATTATGCTGAGCTTTTGTCCAGCTATCTATGATAC 422
 Qy 797 AACAGTACGCTCCTTCAAGAGTTTCCCTGCTCTCTCAATGCTAAGACTCTTCAAGGAGCA 856
 Db 423 AACAGTATTTTCCAGAGATTCGCTTAAACCAAGTCTGCTGATTCCTCAGGAGCA 482
 Qy 857 ACCTTCAGTGTGATGATGATCAATCAAGAGGCAATTTGATGAAGAACTGCGCATACAGA 916
 Db 483 ATCATCAGTTGTATCATGCTCCGCTAATAACCCCAATCAATGAGTGTATGCTTAACCTCGGA 542
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 Qy 976 AACATATGCTGAGGCTACTTTTA 999

Mon Jul 12 10:08:44 2004

us-09-914-098-55.rge

Page 14

Db 603 AACATATAGCAACTGGTCTTTGA 626

Search completed: July 9, 2004, 21:00:24
Job time : 4051 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 18:01:02 ; Search time 467 Seconds
(without alignments)
13626.982 Million cell updates/sec

Title: US-09-914-098-55
Perfect score: 1498
Sequence: 1 gcacgaggttcggttgctg.....aaaaaaaaaaaaaaaaaact 1498

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
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2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1498	100.0	1498	3 AAA64200	Aaa64200 Nucleotid
2	672.8	44.9	1702	3 AAA37472	Aaa37472 DNA enco
3	652.8	43.6	1170	3 AAA37342	Aaa37342 CDNA enco
4	652.8	43.6	1170	3 AAC50510	Aac50510 Arabidops
5	651.4	43.5	1480	3 AAC36124	Aac36124 Arabidops
6	637.4	42.6	1515	2 AAT35205	Aat35205 Limnanthe
7	550.4	36.7	1514	2 AAQ68267	Aaq68267 Maize 2-a
8	549.2	36.7	1632	3 AAA64199	Aaa64199 Nucleotid
9	525	35.0	1415	3 AAA64201	Aaa64201 Nucleotid
10	520.6	34.8	1391	3 AAC50517	Aac50517 Arabidops
11	511.8	34.2	584	3 AAA64183	Aaa64183 Nucleotid
12	491	32.8	1131	3 AAC43080	Aac43080 Arabidops
13	448	29.9	1510	3 AAC43788	Aac43788 Zea mays
14	228	15.2	570	3 AAA64184	Aaa64184 Nucleotid
15	210.8	14.1	485	3 AAC38209	Aac38209 Zea mays
16	193.2	12.9	784	3 AAA64182	Aaa64182 Nucleotid
17	190.6	12.7	312	3 AAA37432	Aaa37432 Maize acy
18	150	10.0	279	3 AAA37433	Aaa37433 Maize acy
19	150	10.0	279	6 ABL73513	Ab173513 Corn tass
20	145	9.7	304	3 AAA37434	Aaa37434 Maize acy
21	132	8.8	259	3 AAA37435	Aaa37435 Maize acy
22	129.4	8.6	235	3 AAA37436	Aaa37436 Maize acy
23	121.8	8.1	1660	3 AAA51068	Aaa51068 Human LPA

24	121.8	8.1	1660	6 AAD24423	Aad24423 Human LPA
25	121.8	8.1	1660	8 ABX16124	Abx16124 Human CDN
26	120.2	8.0	1333	3 AAA71493	Aaa71493 Human lys
27	120.2	8.0	1612	4 AAI60735	Aai60735 Human pol
28	120.2	8.0	1769	4 AAI58949	Aai58949 Human pol
29	120.2	8.0	1769	8 ADB48931	Adb48931 Novel hum
30	120.2	8.0	1832	5 AAH75152	Aah75152 Nucleotid
31	120.2	8.0	1960	6 AAD24014	Aad24014 Human dru
32	120.2	8.0	3059	4 AAD46093	Aad46093 Human DNA
33	120.2	8.0	3060	3 AAA37104	Aaa37104 Human PRO
34	120.2	8.0	3060	4 AAF54413	Aaf54413 Primer #8
35	120.2	8.0	3060	7 ABX78696	Abx78696 Human PRO
36	120.2	8.0	3060	7 ACA75668	Aca75668 Novel hum
37	120.2	8.0	3060	7 ACA71148	ACA71148 Human sec
38	120.2	8.0	3060	7 ACC87676	Acc87676 Human sec
39	120.2	8.0	3060	7 ACC87062	Acc87062 Human sec
40	120.2	8.0	3060	7 ACD04235	Acd04235 Human sec
41	120.2	8.0	3060	7 ACA69566	ACA69566 CDNA enco
42	120.2	8.0	3060	7 ACA90411	Aca90411 Novel hum
43	120.2	8.0	3060	7 ACC89518	Acc89518 Human sec
44	120.2	8.0	3060	7 ACA98309	Aca98309 Novel hum
45	120.2	8.0	3060	7 ACA93951	Aca93951 Human sec

ALIGNMENTS

RESULT 1
AAA64200
ID AAA64200 standard; DNA; 1498 BP.
XX
AC AAA64200;
XX
DT 20-DEC-2000 (first entry)
XX
DE Nucleotide sequence of a lysophosphatidic acid acetyltransferase.
XX
KW Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;
KW triacylglycerol; oil content; ss.
XX
OS Glycine max.
XX
FH Key
CDS Location/Qualifiers
FT 126..1259
FT /*tag= a
FT /product= "lysophosphatidic acid acetyltransferase
FT (LPAAT) isoenzyme"
XX
PN WO200049156-A2.
XX
PD 24-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-US004526.
XX
PR 22-FEB-1999; 99US-0121119P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;
DR WPI; 2000-558300/51.
DR P-PSDB; AAB08478.
XX
FT New nucleic acid fragment encoding a lysophosphatidic acid
FT acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants
FT which encode LPAAT at higher or lower levels than normal.

Claim 39; Page 99; 102pp; English.
XX
CC The present sequence encodes a lysophosphatidic acid acetyltransferase
CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic
CC plants which encode LPAAT at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found.

PA (CALJ) CALGENE LLC.
 PT Lasner MW, Emig RA, Ruerinsky DM, Van Benennaam A;
 PI WPI; 2000-303447/26.
 DR P-PSDB; AAY99473.
 XX Novel acyltransferase related proteins useful for altering membrane fluidity in plant cells e.g. to induce chill tolerance.
 PT Example 5; Page 74-75; 126pp; English.
 XX The invention relates to nucleic acids encoding novel plant acyltransferase-like proteins (AA37343-A37445; which comprise one of 8 conserved acyltransferase motifs (AAY99474-Y99481). Acyltransferases catalyze the transfer of acyl groups from a donor to a variety of substrates such as glycerides, sterols, stanols and phosphatides. Such enzymes play a key role in lipid synthesis, and thereby affect the characteristics of the plant. For example, cold-hardened plants have different lipid concentrations in the cell membrane compared to non-hardened plants, which makes the membrane more fluid and the plant more tolerant of low temperatures. The nucleic acid sequences of the invention can be used as probes or for expressing acyltransferase-like proteins in host cells e.g. for recombinant protein production. They may be expressed in plant cells to alter the lipid composition of the plant e.g., for the production of chill-resistant plants, or for altering the composition of plant oils. Sequences AA37331-A37342 represent cDNAs encoding Arabidopsis thaliana acyltransferases ATAT1-ATAT11 and lysophosphatidic acid acyltransferase ATL2PANT1, respectively.
 XX Sequence 1170 BP; 306 A; 277 C; 268 G; 319 T; 0 U; 0 Other;
 SQ

Query Match 43.6%; Score 652.8; DB 3; Length 1170;
 Best Local Similarity 74.2%; Pred. No. 2.8e-160;
 Matches 825; Conservative 0; Mismatches 287; Indels 0; Gaps 0;

QY 138 GCACGGCGGTGGTGGTACCATTTGGGCTCTCTCTCTCCCTCCGCTCCCTGTTAAT 197
 DB 10 GCTGACGCTGTCGTCGCTTTGGGCTTCTCTCTCTCATATCTGCTCTGCTGCAAT 69
 QY 198 CTCAATCAGCAATATGCTATGCTGCTGTAAGCCGCTGTCGAAAGTTTGTACAGAAG 257
 DB 70 CTCTTTTCCAGGAGTTTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 129
 QY 258 ATCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317
 DB 130 ATTAAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 189
 QY 318 GCAGGAGTTAAGTTCCTCAATTTTACAGATCATGAACCTTTCTGTTAATGGTAAAGAG 377
 DB 190 GCTGGAGTTAAGTTCCTCAATTTTACAGATCATGAACCTTTCTGTTAATGGTAAAGAG 249
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 DB 250 CATGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
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 DB 370 CTTCAGTCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429
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 DB 790 GACGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 849
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 DB 850 CACATAGCTGCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 909
 QY 1038 TCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1097
 DB 910 TCCCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969
 QY 1098 CAATGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1157
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 QY 1158 GTTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1217
 DB 1030 ATCATCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1089
 QY 1218 GCCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1249
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RESULT 4
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 XX 18-OCT-2000 (first entry)
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 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 XX promoter; termination sequence; ss.
 OS Arabidopsis thaliana.
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Qy	342	ACGATCATGAACCTTCCTTTAATGGTAAAGAGCATGCACTTGTGTAAAGCAATCAC	401
Dd	389	GCTGATGACAAATCTTACAGGCAATGGGAATGAGCATGCACTTGTCAATCAATAAT	448
Qy	402	AGAAGTGATATTGATTTGGCTTGTGGATGGTTTCAGCTCAGCGTTTCAGTTTGTCTGGC	461
Dd	449	CGGAGCGATATCGATTGGCTTATTTGGTGGATTGGTGGCAGCGCTCAGGATGCCTTGA	508
Qy	462	AGCACTCTAGCTGTGATGAAGAATCTTCAAGTCTTCTGCCGTCATTCGGCTGGTCAGT	521
Dd	509	AGTACACTCTCTCTTATGAAGAATCATCGAAATCTTCCAGTTATTTGGCTGGTCCATG	568
Qy	522	TGTTTTCTCAGTATCTTTTCTGGAGAGAAATTTGGCCAAAGATGAAGCAATTAAG	581
Dd	569	TGTTTTGCAGATACCTTTTGGAAAGAGCTGGGCAAGGATGAAGCAATTAAG	628
Qy	582	TCAGGCATCCAGGAGCTGATGATTTCCCTCTCTTCCCTTTGGCTAGCTCTCTTTAGAA	641
Dd	629	TGGGGCTCCAAAGTTGAAGGATCTCCCGAGACCAATTTTGGCTAGCCCTTTTGTGAG	688
Qy	642	GGACGCGTTTACACAGGCCAACTATTAGCTGCTCAGGAATATGCCATTCCTCACTGA	701
Dd	689	GGCACTCGCTTTACTCAGCAAGAGCTTCTAGCAGCTCAGGATATGCTGTTTACAGG	748
Qy	702	TTGCTGTTCTAGAAATGTTTGAATCCAAAGCAATGAAGTTTGTCTGCTGAGTAAGT	761
Dd	749	TTGCCAGCACCCAGAAATGATTGATTCACGCTACAAAGGAAATTTGATCAGCTGTAAT	808
Qy	762	CATATGGCTCATTGTTCTCGCANTTATGATGATACAGTAGCCATCCCTAAGATTC	821
Dd	809	ATTATGGGGATTTTGTTCAGCTATTATGATACACAGATTAATTTCCAAAGATTC	868
Qy	822	CTGCTCTCAATGCTAAGACTCTTCAAGGCAACCTTCAGTGGTGCATGTTTATATC	881
Dd	869	CCTCAACCAACATGCTCGGATTTTGAAGGGCAATCTTCAGTGGTACATGTTGCATG	928
Qy	882	AAGAGGATTTGATGAAGGAACTCCAGATACAGATGAGCTGTTGCTCAATGGTTCGA	941
Dd	929	AAAGCTCATGATGATGATGATGCCAAAGTCAAGAGCAGATGTTTCAAAATGGTCAAA	988
Qy	942	GATATATTTGGCCCAAGGATGCTTCTGTAGACAAACATATGGCTGAGGCTACTTTAGT	1001
Dd	989	GACATCTTTGACAAAGGATGCAATTAAGTATGATGATGATGATGATGATGATGATG	1045
Qy	1002	GATCAAGAGCTGACGATGATGCTGACCAATTAAGTCTCTTCTGGTATGATTAATCTGG	1061
Dd	1046	GATGAGGATATGACCAATTTGGCGGCCAGTAAATCAATTTGCTGATGATGATGATG	1105
Qy	1062	GCCTGCTGCTGTTGTGGGGTCTGTAAGTTCTGCAATGGTCTTCTGTTACTCTCTTC	1121
Dd	1106	TCATGCTCTCTTTTATATGGCGCGTCAAGCTCTTCTATGGAATCACTCTCTGTCACA	1165
Qy	1122	TGAAGGGTGTGTCATTTTACGCTTTTGGTTTGGCAGTTGTTATGTCACATTAATGCAAT	1181
Dd	1166	TGGAAGGAGTCGGTTTACGGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1225
Qy	1182	CTGATTCATTTCTCAGCTGACAGGTTTCAACCCGGCCAG	1233
Dd	1226	TTTCATCATGTTCTCGCAGTCAGCGATCGAGCTCAGGCTCAGCCAG	1267
RESULT 9			
AAA64201			
ID	AAA64201 standard; DNA; 1415 BP.		
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AC	AAA64201;		
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DT	20-DEC-2000 (first entry)		

XX Nucleotide sequence of a lysophosphatidic acid acetyltransferase.
DE Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;
KW triacylglycerol; oil content; ss.
OS Triticum aestivum.
XX Location/Qualifiers
FH 30..1154
FT /*tag= a
FT /product= "lysophosphatidic acid acetyltransferase
FT (LPAAT) isoenzyme"
XX WO200049156-A2.
PN 24-AUG-2000.
XX 22-FEB-2000; 2000WO-US004526.
XX 22-FEB-1999; 99US-012111199.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;
XX P-PSDB; AAB08479..
XX WPI: 2000-558300/51.
XX New nucleic acid fragment encoding a lysophosphatidic acid
PT acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants
PT which encode LPAAT at higher or lower levels than normal.
XX Claim 39; Page 101; 102pp; English.
XX The present sequence encodes a lysophosphatidic acid acetyltransferase
CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic
CC plants which encode LPAAT at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found.
CC This would have the effect of altering the level of specific
CC triacylglycerols in those cells, for e.g. overexpression of an LPAAT
CC similar to the maize LPAAT will result in higher oil content in the seed,
CC stem and leaf. LPAAT chimeric genes may be used for co-suppression of
CC genes encoding LPAAT. The polynucleotides may also be used as probes for
CC Genetically and physically mapping the genes that are a part of, and as
CC markers for traits linked to those genes
XX Sequence 1415 BP; 365 A; 299 C; 341 G; 410 T; 0 U; 0 Other;
SQ

Query Match 35.0%; Score 525; DB 3; Length 1415;
Best Local Similarity 67.7%; Pred. No. 8.4e-127;
Matches 751; Conservative 0; Mismatches 355; Indels 3; Gaps 1;
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Dd 18 GGGGGGGGGCCATGGCGATTCCTCGTCTGCTCTCCCTCCGCTCGGCTCTCTTC 77
QY 174 TTGCGCTCGGCTCCTTGTATCTCATTCAGGCAATATGCTATGCTGCTAAGGCGG 233
Dd 78 CTCCTCTCGGCTCGTCTGTCACACTGTCCAGGCGGTATTGTTCTTGACGATAGGCCA 137
QY 234 GTGTGCAAAAGTTGTACAGAGGATCAACCGGGTAGTAGCAGAGCTTTTGGCTGGAG 293
Dd 138 TTCTCGAAGCGATTGTACCGGAGATCAACGTATTCTCTCGGCGAGTTGTTGGCTTCAG 197
QY 294 CTGTATGCTTATTGATTGGTGGCAGGAGTTAAGTCCAAATATTCACATCATGAA 353
Dd 198 CTGATCTGGCTTGTGGACTGGTGGGCGAGGTATTAAGGTACAGGTGTATCGGATCCAGAA 257
QY 354 ACCTTTCTGTTTAAATGGTAAAGCATGCACTTGTGATAAGCAATCACAAGATGATATT 413
Dd 258 ACTTGGAAACTAATGGGCAAGAGCACGCCCTTCTCATATCCATCATCAAGTGCATT 317

QY 414 GATTGGCTTGTGGATGGTTTACGCTCAGCGTTTCTAGTGTCTTGGCAGCACTCTAGCT 473
Db 318 GATTGGCTGGTGGATGGTTTATGACACAGCGTTTCTAGTGTCTTGGCAGCACTCTAGCT 377
QY 474 GTGATGAAGAATCTTCAAGATTTCTGCGGCTCATTTGGCTGGTCAATGTGTTTCTGAG 533
Db 378 ATAATGAAGAATCTTCAAGATTTCTGCGGCTCATTTGGCTGGTCAATGTGTTTCTGAG 437
QY 534 TATCTTTTCTGAGAGAGTGGCCCAAGATGAAGCAATTAAGTCAAGGATCCAG 593
Db 438 TACCTCTTTTGGAGAGAGTGGCCCAAGATGAAGCAATTAAGTCAAGGATCCAG 497
QY 594 CGACTGAGTATTTCCCTTTCCCTTTTGGCTAGCTCTTTTGGAGGAGCAAGCGTTT 653
Db 498 AGGTTGAAGACTTCCCGAGATCAATTTGGCTGCCCTTTTGGAGGAGCAAGATTT 557
QY 654 ACACAGGCCAAATATTAGTGTCTCAGGAATATGCCACTTCCACTGATTCCTTCTCT 713
Db 558 ACTCCAGCAAACTTTTAGCAGCTCAAGATATGCACTCTCACAGGCTTTGACAGCGCT 617
QY 714 AGAATGTTTGTATTCAGCAAGCTAAGGTTTGTCTTCTGAGTCAATATCGGCTCA 773
Db 618 AGAATGTTTGTATTCAGCAAGCTAAGGTTTGTCTTCTGAGTCAATATCGGCTCA 677
QY 774 TTTGTTCTGCAATTTATGATTAACAGTAGCCATCCCTAAGAGTTCCCTGCTCTCTACA 833
Db 678 TTTGTTCTGCAATTTATGATTAACAGTAGCCATCCCTAAGAGTTCCCTGCTCTCTACA 737
QY 834 ATGCTAAGCTTCTCAAGGACCACTTCTGAGTGTGATTTTCAATCAAGAGGCAATTTG 893
Db 738 ATGCTGCTATTTCTCAGGACCAATCATCAGTTGTTTCAATGCTCCGATCAAAACGCTCA 797
QY 894 ATGAAGGAATGCCAGATACAGATGAGCTGTTGCTCAATGGTGTGAGATATATTTTG 953
Db 798 ATGAGTATATGCTTACTCGGATGAGGATGTTTCAAAATGGTGTGAGATATATTTTG 857
QY 954 GCCAAGGATGTTTGTAGCAACAATATGCTGAGGTTACTTTTATGATCAAGAGCTG 1013
Db 858 GCCAAGGATGTTTGTAGCAACAATATGCTGAGGTTACTTTTATGATCAAGAGCTG 914
QY 1014 CAGGATATGCTGACCAATTAAGTCTTCTGAGTGTGATTTTATGATCAAGAGCTG 1073
Db 915 ATACCAATGCTGCTGAGTGAATCTTTGAGGTTGCTGCTGCTGCTGCTGCTGCTC 974
QY 1074 GTTGGGGGTCTGAAAGTTCTGCAATGCTTCTGCTTCTCTTCTGGAAGGTTGTT 1133
Db 975 CTATATGCTGCTCATAGATTTCTACAGTGGACCCAGCTTTGCGACGTGGAAGAGTG 1034
QY 1134 GCATTTTCACTTTTGTGTTGGCAGTTGTACTGCACTTATGCAATTTCTGATTCATTC 1193
Db 1035 ATCTCTTTTCTGATTTGGCAATGTTAAGCGGTTATGCAATGATTCATCATGTTTC 1094
QY 1194 TCACAGTCAGAGGTTTCAAAACCGGCCAA 1222
Db 1095 TCGAGCCGAGCGCTCAAGCTCTGCGAA 1123

RESULT 10

AAC50517
ID AAC50517 standard; DNA; 1391 BP.
XX AAC50517;
AC AAC50517;
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 65136.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65136.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX

PN BP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
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PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
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PR 14-MAY-1999; 99US-0134370P.
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PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136382P.
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PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140895P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.

Query Match 34.8%; Score 520.6; DB 3; Length 1391;

558 GCCAAGGATGAAGCACAATTAAAGTCAGGCATCCAGCACTGAGTGATTTCCCTCTTCCC 617
 665 GCCAAGGATGAAGCACAATTAAAGTCAGGCATCCAGCACTGAGTGATTTCCCTCTTCCC 724
 618 TTTTGGCTAGCTCTTTTGTAGAGGAACGGTGTTCACAGGCCAACTATTAGTGCT 677
 725 TTCTGTTAGCCCTTTTGTGAGGGAACCTGCTTTACAGAGCCAACTTAAAGCCGCA 784
 678 CAGGAATATGCCACTTCCACTGGATTGCTTCTTCTAGAAATGTTTGTATTCAGAACT 737
 785 CAAGAGATGAGCCTCTCTGAATTGCTTATCCCTCGAATGTTGATTTCTCGCACC 844
 738 AAGGGTTTGTCTGAGTAAGTCATATGCGCTCATTTGCTGCTCATTTATGATGA 797
 845 AAAGGTTTGTGTCAGCTGTTAGTAATATGCTTTCATTTGCTCCAGCAATTTATGATG 904
 798 ACAGTAGCCATCCCTAAGAGTCCCTGCTTCTACATGCTAAGACTTCAAGGACAA 857
 905 ACAGTAGCTATTCAGAAACCTTCCACACCCACGATGCTAAGACTTCAAGGACAA 964
 858 CCTTCAGTGTGCTATTCATACAGAGGCAATTTGATGAAGGAACCTGCCAGATACAGAT 917
 965 CCTTCAGTGTGCTATTCATACAGTGTCACTCGATGAAGACTTACCTGAATCAGAT 1024
 918 GAGGCTGTTGCTCAATGCTCGAGATATATTTGTGCCCAGGATGCTTTGTTA 971
 1025 GACCAATTGACAGTGTGAGAGATCAGTTTGTGCTAAGGTGTTCTATCA 1078

RESULT 11
 ID AAA64183
 AC AAA64183;

20-DEC-2000 (first entry)

Nucleotide sequence of a lysophosphatidic acid acetyltransferase.

Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;

triacylglycerol; oil content; ss.

Glycine max.

Key Location/Qualifiers

CDS 114..461

/tag= a

/product= "lysophosphatidic acid acetyltransferase"

(LPAAT) isoenzyme"

/note= "no termination codon given"

W0200049156-A2.

24-AUG-2000.

22-FEB-2000; 2000MO-US0004526.

22-FEB-1999; 99US-0121119P.

(DUPO) DU PONT DE NEMOURS & CO E I.

Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;

WPI; 2000-558300/51.

P-PSDB; AAB08461.

New nucleic acid fragment encoding a lysophosphatidic acid

acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants

which encode LPAAT at higher or lower levels than normal.

CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic
 CC plants which encode LPAAT at higher or lower levels than normal or in
 CC cell types or developmental stages in which they are not normally found.
 CC This would have the effect of altering the level of specific
 CC triacylglycerols in those cells, for e.g. overexpression of an LPAAT
 CC similar to the maize LPAAT will result in higher oil content in the seed,
 CC stem and leaf. LPAAT chimeric genes may be used for co-suppression of
 CC genes encoding LPAAT. The polynucleotides may also be used as probes for
 CC genetical and physically mapping the genes that are a part of, and as
 CC markers for traits linked to those genes
 XX

SQ Sequence 584 BP; 114 A; 116 C; 170 G; 175 T; 0 U; 9 Other;

Query Match 34.2%; Score 511.8; DB 3; Length 584;

Best Local Similarity 95.0%; Pred. No. 1.6e-123;

Matches 555; Conservative 0; Mismatches 26; Indels 3; Gaps 3;

QY 12 CTTTTGCTGACCTGACCTCGGAATCCAAAGAGAGGAACTCAAGTGTTCGTTGCGTTG 71
 Db 1 CTTTTGCTGACCTGACNNCGGTTTTTTTTTTNGG-GGNNCACGCTGTTGTTGCGTTG 59
 QY 72 TGCTCTGCTCTGCTCTCTTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 131
 Db 60 TGCTCTGCTCTGCTCTCTTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 119
 QY 132 ATTGCAGCAGCGGCGTGTGTGTACCATTTGGGCTGCTCTTTTCGCTCCGCGCTCCTT 191
 Db 120 ATTGCAGCAGCGGCGTGTGTGTACCATTTGGGCTGCTCTTTTCGCTCCGCGCTCCTT 179
 QY 192 GTTAATCTCATTTGAGCAATATGCTATGCTGCTAAGGCGGCTGTCGAAAGTTGTATC 251
 Db 180 GTTAATCTCATTTGAGCAATATGCTATGCTGCTAAGGCGGCTGTCGAAAGTTGTATC 239
 QY 252 AGAAGGATCAACCGGCTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGTATGGCTTATTGAT 311
 Db 240 AGAAGGATCAACCGGCTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGTATGGCTTATTGAT 299
 QY 312 TGGTGGCAGGAGTTAAGTCCAAATATTCACAGATCATGAAACCTTTTCGTTTAAATGGGT 371
 Db 300 TGGTGGCAGGAGTTAAGTCCAAATATTCACAGATCATGAAACCTTTTCGTTTAAATGGGT 359
 QY 372 AAAGAGCATGCATCTGTGTATAAGCAATCAGAAAGTATATTCATTTGGCTTGTGGATGG 431
 Db 360 AAAGAGCATGCATCTGTGTATAAGCAATCAGAAAGTATATTCATTTGGCTTGTGGATGG 419
 QY 432 GTTTCAGCTCAGGCTTCAGTTGTCTTTGGCAGACTCT-AGCTGTGATGAAGAAATCTTC 490
 Db 420 GTTTCAGCTCAGGCTTCAGTTGTCTTTGGCAGACTCTAAGCTGTGATGAAGAAATCTTC 479
 QY 491 AAAGTTTCTGCCGCTCATTCGCTGGTCAATGTGGTCTTCTGAGTATCTTTTCTGGAG-A 549
 Db 480 AAAGTTTCTGCCGCTCATTCGCTGGTCAATGTGGTCTTCTGAGTATCTTTTCTGGAG-A 539
 QY 550 GAAGTTGGCCAAAGGATGAAGCAATTAAGTCAGGCATCCAG 593
 Db 540 GAAGTTGGCCAAAGGATGAAGCAATTAAGTCAGGCATCCAG 583

RESULT 12

AAC43080

ID AAC43080 standard; DNA; 1131 BP.

XX AAC43080;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 37952.

XX Hybridisation assay; genetic mapping; gene expression control;

XX protein identification; signal transduction pathway; metabolic pathway;

XX promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX	EP1033405-A2.	PR	01-JUL-1999;	99US-0141842P.
PN		PR	01-JUL-1999;	99US-0142154P.
XX		PR	02-JUL-1999;	99US-0142055P.
PD		PR	06-JUL-1999;	99US-0142390P.
XX	06-SEP-2000.	PR	08-JUL-1999;	99US-0142803P.
PF		PR	09-JUL-1999;	99US-0142820P.
XX	25-FEB-2000; 2000EP-00301439.	PR	12-JUL-1999;	99US-0142977P.
XX		PR	13-JUL-1999;	99US-0143542P.
PR	25-FEB-1999;	PR	14-JUL-1999;	99US-0144005P.
PR	05-MAR-1999;	PR	15-JUL-1999;	99US-0144085P.
PR	09-MAR-1999;	PR	16-JUL-1999;	99US-0144086P.
PR	23-MAR-1999;	PR	19-JUL-1999;	99US-0144325P.
PR	25-MAR-1999;	PR	19-JUL-1999;	99US-0144331P.
PR	29-MAR-1999;	PR	19-JUL-1999;	99US-0144332P.
PR	01-APR-1999;	PR	19-JUL-1999;	99US-0144333P.
PR	06-APR-1999;	PR	19-JUL-1999;	99US-0144334P.
PR	08-APR-1999;	PR	19-JUL-1999;	99US-0144335P.
PR	16-APR-1999;	PR	20-JUL-1999;	99US-0144352P.
PR	19-APR-1999;	PR	20-JUL-1999;	99US-0144632P.
PR	21-APR-1999;	PR	20-JUL-1999;	99US-0144884P.
PR	23-APR-1999;	PR	21-JUL-1999;	99US-0144814P.
PR	28-APR-1999;	PR	21-JUL-1999;	99US-0145086P.
PR	30-APR-1999;	PR	21-JUL-1999;	99US-0145085P.
PR	30-APR-1999;	PR	22-JUL-1999;	99US-0145087P.
PR	04-MAY-1999;	PR	22-JUL-1999;	99US-0145089P.
PR	05-MAY-1999;	PR	22-JUL-1999;	99US-0145152P.
PR	06-MAY-1999;	PR	22-JUL-1999;	99US-0145152P.
PR	07-MAY-1999;	PR	23-JUL-1999;	99US-0145218P.
PR	07-MAY-1999;	PR	23-JUL-1999;	99US-0145218P.
PR	11-MAY-1999;	PR	23-JUL-1999;	99US-0145224P.
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PR	18-MAY-1999;	PR	27-JUL-1999;	99US-0145919P.
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PR	19-MAY-1999;	PR	02-AUG-1999;	99US-0146386P.
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PR	01-JUN-1999;	PR	05-AUG-1999;	99US-0147192P.
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PR	08-JUN-1999;	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	PR	10-AUG-1999;	99US-0148171P.
PR	10-JUN-1999;	PR	11-AUG-1999;	99US-0148319P.
PR	14-JUN-1999;	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	PR	23-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	PR	23-AUG-1999;	99US-0149930P.
PR	18-JUN-1999;	PR	25-AUG-1999;	99US-0150566P.
PR	18-JUN-1999;	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	PR	27-AUG-1999;	99US-0151065P.
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PR	18-JUN-1999;	PR	27-AUG-1999;	99US-0151080P.
PR	21-JUN-1999;	PR	30-AUG-1999;	99US-0151303P.
PR	22-JUN-1999;	PR	31-AUG-1999;	99US-0151438P.
PR	23-JUN-1999;	PR	01-SEP-1999;	99US-0151930P.
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PR	29-JUN-1999;	PR	15-SEP-1999;	99US-0154018P.
PR	30-JUN-1999;			

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PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
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PR 25-OCT-1999; 99US-0161404P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      32.8%; Score 491; DB 3; Length 1131;
Best Local Similarity 85.4%; Pred. No. 6e-118;
Matches 719; Conservative 0; Mismatches 380; Indels 0; Gaps 0;

QY 126 ATGGCTATTGACAGCGGCGGTGGTGGTACCAATGGGCGTCTCTCTCTTCGCTCCGGC 185
DB 1 ATGAAGATCCCTGCGGCTCTTGCTTTATCCCTGTGGTGCTCTCTTGATCTCAGG 60

QY 186 CTCCTTGTTAACTCTATTCAGGCAATATGCTATGCTGCTGAAGCGGCTGCAAAAGT 245
DB 61 CTCATCTCAACATCAATTCAGCTTGTTCTTCATCAATGTTTCGTCCTCAAGAAAGT 120

QY 246 TTGTCAGAGAGGATCAACCGGTAGTACAGAGCTCTTGCTGGCTGAGCTTGATGGCTT 305
DB 121 TTGATAGAGATTAACAANAATGTTGCGGAATACITTTGTTGAGCTCATATGGT 180

QY 306 ATGATGTTGGGACAGGATTAAGTTCACAAATATTACAGATCATGAACCTTTCTGTTA 365
DB 181 TTGATGTTGGGCTTGTTAAAGATCAATTTATACGTCGATGACAGACTCTAGAGTTA 240

QY 366 ATGGGTAAGAGCATGCTCTGTGTAAGCAATCAAGAGTGATATTCATGCTGCTT 425
DB 241 ATGGGAAAGAACACGCACTTGCTTTAGCAATCATCGAAGTGACATGATGGCTTAT 300

QY 426 GGATGGTTTACGCTCAGGCTTTCAGGTTGCTTTGGCAGCACTCTAGCTGTGATGAAGAA 485
DB 301 GGATGGGTCATGGCTCAGGCTTAGGTTGCTTTGGAAGCTCATTAGCCATCATGAAGAA 360

QY 486 TCTTCAAGTTTCTCGCGGTGATGCTGGTCAATGCTGTTTCTGAGTATCTTTTCTG 545
DB 361 GAAGCAAGTATCTTCCAAATACATAGTTGGTGGATGCTGTTTTCGGATTACATTTCTG 420

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QY 546 GAGAGAAGTTGGGCAAGGATGAAGACACATTAAGTCAGGCATCCAGCGACTGAGTAT 605
DB 421 GAAAGAAGTTGGGCTAAAGATGAGATACCCCTCAAGCGAGGTTTAAACGACTTGAAGAC 480
QY 606 TTCCCTCTTCCTTTGGCTAGCTCTCTTTGTAGAGGAACGCGTTTACACAGGCCAAA 665
DB 481 TTTCCAATGACATTTGGTTAGCTCTTTTCGTTGAAGGAACTCGTTTCACTCAGGAGAAG 540
QY 666 CTATTAGCTGCTCAGGAATATGCCACTTCCACTCGATTGCTGTTCTAGAAATGTTTTG 725
DB 541 CTGGAAGCTGCTCAAGAGTACGCTCTATCAGAAGCTTACCGTCTCTCGAAATGTTTTG 600
QY 726 ATTCCAGAACTAAGGGTTTGGTTTCTGCGAGTAAGTCAATATGCGCTCATTTGTCCTGCC 785
DB 601 ATTCCTCGTACAAAGGATTTGTTTCGCGAGTGTCTGAAATACGGTCAATTTGTTCTGCA 660
QY 786 ATTTATGATGTAAACAGTAGCCATCCCTAAGAGTTCCCTGCTCCTCAAAATGCTAAGACTC 845
DB 661 ATATATGACTGTACTTAAACCGTTCAATACAGCTACACCACTCTGCTTAGGATG 720
QY 846 TTCAAGGGAACAACTTCAGTGGTGCATGTTTATATCAAGAGGCAATTTGATGAAGGAATG 905
DB 721 TTCAGTGGACAATCATCTGAGATAAATTTGAGATGAGAGCTCACAAATGAGTGAGTTG 780
QY 906 CCAGATACAGATGAGGCTGTTGCTCAATGCTGCGAGATATATTTGGGCCAAGGATGCT 965
DB 781 CCAGAAACCGATGATGGCATTTGCAATGGTGCCAGATCTATTTATCACCAAGGATGCT 840
QY 966 TTGTTAGACAAACATATGCTGAGGTTACTTTTAGTGATCAAGAGCTGCAGGATCTGGT 1025
DB 841 CAACTTCAGAAATACTTTCACAAAAGACGTTTTCAGCGACTTGAAGTTCACCAATTAAC 900
QY 1026 CGACCAATAAGTCTCTCTGTTAGTTATATCTTGGCGGTGCTGTTGTTGGGGGTCT 1085
DB 901 CGGCCAATCAAGCCATTAATCGTGGTCAATCAITGGTTAGGTTTCTCTGTTATTCGGTGGT 960
QY 1086 GTAAAGTTCTCTCAATGCTCTCTGTTACTCTCTCTTGGAAAGGTTGTTGATTTTCAGCT 1145
DB 961 TTCAGCTACTGCAATGCTTTCAATAGTGGCTCTGTTGAGATCATCTCTTTGTTGTTG 1020
QY 1146 TTGCTTTGGCAGTTGTTACTGCACTTATGCAAAATTCGATTAATTCACAGTCAGAG 1205
DB 1021 TTCTTCTTGTCTATGCACTATAACAATGCAAAATCTATTTCAATCGTCTGAGTCACAA 1080
QY 1206 CGTTCAAAACCGGCCAAGA 1224
DB 1081 CGTTCAACTCCAGCCCAAGA 1099

RESULT 13
AAC43788
ID AAC43788 standard; DNA; 1510 BP.
XX AC AAC43788;
XX AC AAC43788;
XX DT 18-OCT-2000 (first entry)
XX Zea mays DNA fragment SEQ ID NO: 40518.
XX Zea mays DNA fragment SEQ ID NO: 40518.
XX Hybridisation assay; generic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic; pathway;
XX promoter; termination sequence; corn; ss.
XX Zea mays subsp. mays.
XX EPI033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000BP-00301439.
XX 25-FEB-1999; 99US-0121825P.

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PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-01223548P.
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CC This would have the effect of altering the level of specific
CC triacylglycerols in those cells, for e.g. overexpression of an LPAAT
CC similar to the maize LPAAT will result in higher oil content in the seed,
CC stem and leaf. LPAAT chimeric genes may be used for co-suppression of
CC genes encoding LPAAT. The polynucleotides may also be used as probes for
CC genetically and physically mapping the genes that are a part of, and as
CC markers for traits linked to those genes
XX
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Query Match 15.2%; Score 228; DB 3; Length 570;
Best Local Similarity 70.2%; Pred. No. 2.9e-49;
Matches 306; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

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Search completed: July 9, 2004, 19:52:37
Job time : 472 secs

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RESULT 2

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; Patent No. 5843739
; GENERAL INFORMATION:
; APPLICANT: SLABAS, ANTONI R.
; APPLICANT: BROWN, ADRIAN P.
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,267
; FILING DATE: 08-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02528
; FILING DATE: 10-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1514 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 130..1254
US-08-454-267-1

Query Match 36.6%; Score 548.8; DB 2; Length 1514;
Best Local Similarity 68.8%; Pred. No. 3.1e-158;
Matches 770; Conservative 0; Mismatches 347; Indels 3; Gaps 1;
Qy 104 GCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 163
Db 108 GCGGCG 167
Qy 164 CTTGCTCTTCTGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 223
Db 168 CTTGCTCTTCTGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 227
Qy 224 CGTAAGCCCGGTGTGAAAAAGTTTGTACAGAAGATCAACCGGGTAGTAGCAG 283
Db 228 GATAAGCCCTTTTTCGAAGAGCTTACCGTCGGATCAACAGATTCTTGGCCGAG 287
Qy 284 GTGGCTGGAGCTGTATGCTTATGATTGGTGGGAGAGTTAAGTCCAAATATTC 343
Db 288 GTGGCTTCAGCTGTCTGGGTGGGAGTGGTGGGAGTGGTGGGAGTGGTGGGAG 347
Qy 344 AGATCATGAACCTTTTCTGTTTAAATGGGTAAGAGAGCATGCACTTGTGATA 403
Db 348 AGATGAGNAACCTTACAGATCAATGGGTAAGAGAGCATGCACTCATATCA 407

Db 888 ACCTCATGCAATGAGTGCAGATGCCAAATACATGAGGATGTTTCAAAATGGTGTAAAGA 947
QY 944 TATATTGTGGCAAGATGCTTTTGTAGACAAAATATGCTGAGGGTACTTTTAGTGA 1003
Db 948 CATTTTGTGGAAAGATGCTTTACTGACAAAGCATTTTGGCAACAGGACATTT---CGA 1004
QY 1004 TCAAGAGCTGCAGGATGCTGACCAATAAAGTCTCTCTGGTAGTTATATCTTGGGC 1063
Db 1005 TGAGGAGATTAGACCTATTGGCCGCTCCAGTGAATCATTTGCTGGTGAACCTGTTCTGTC 1064
QY 1064 GTGTCTGGTGTGTGGCGGTCTGTAAAGTTCCTGCAATGGTCTTCTGTTACTCTCTCTG 1123
Db 1065 GTGCCCTCTGCTTTTGGCGCATCGAGTTCTTCAAGTGGACACAGCTTCTGTCAGCGTG 1124
QY 1124 GAAGGCTGTGCATTTTCAAGCTTTTGGTTGGCAGTTGTACTGACATATGCAATTTCT 1183
Db 1125 GAGGCTGTGGCGTTTCACTGCCGAGGATGGCGTTTGTGACGGGTGTATCATGTCTT 1184
QY 1184 GATTCAATTCTCACAGTCAAGAGCTTCAAAACCGGCCAAG 1223
Db 1185 CATCATGTTCTCCAGGCTGAGCGGTGAGCTCAGCCAGG 1224

RESULT 5

US-09-215-252-12
; Sequence 12, Application US/09215252
; Patent No. 6300487
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: ADUREL, DANIEL
; APPLICANT: HOLLENBACK, DANIEL
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0151
; CURRENT APPLICATION NUMBER: US/09/215,252
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (184)..(1311)
US-09-215-252-12

Query Match 8.1%; Score 121.8; DB 4; Length 1660;
Best Local Similarity 46.9%; Pred. No. 6.5e-27;
Matches 415; Conservative 0; Mismatches 467; Indels 3; Gaps 1;
QY 146 CGTGGTGGTACCATTTGGCGCTCTCTCTGGCTCCGGCTCTTTGTTAACTCATTC 205
Db 216 CGTCTGCACCTCTGCTGGCTTTGCTCTGTTGAGTGGTCTGTTCACTCAACTTCT 275
QY 206 GGCATATGCTATGCTGTAAAGCGGTGTGAAAAGTTGTACAGAGATCAACCG 265
Db 276 CCAGCTGTGCACGCTGGCGCTCTGGCGGTTCAGACAGCTCTACCGCGCTCAACTG 335
QY 266 GGTATGACAGAGCTCTTGGCTGGAGCTTGTATGCTTATTGTTGGGCGAGGT 325
Db 336 CCGCTCGCATATCTACTCTGGAGCCACTGCTCATGCTGCTGGAGTGTGTTCTGAC 395
QY 326 TAAGGTCCAATATTCAGATCATGAAACCTTTCGTTTAAAGGTAAGAGATGCACT 385
Db 396 GGAAGTGTACACTGTTACCGACCCAGGCCAGGTAGAGCGCTTTGGGAAGGAGCACGCT 455
QY 386 TGTGATTAAGCAATACAGAGATGATATTGTTGGCTTGTGGTGGTTTCAGCTCAGCG 445
Db 456 CATCATCTCAACACAACTTCAGATCGACTTCTCTGTGGGTGGACCATGTTGAGCG 515
QY 446 TTCAGGTTGCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCCGT 505

Db 516 CTTGGAGTGTGGGAGCTCCAAAGTCTCGCTAAGAGAGCTGCTCTACGTGCCCT 575
QY 506 CATTTGCTGTGCAATGTTGTTCTGAGTATCTTTTCTGAGAGAAAGTTGGGCAAGGA 565
Db 576 CATCGCTGACGTGGTACTTTCTGGAGATTGTTCTGCAAGCGGAAGTGGAGGAGGA 635
QY 566 TGAAGCACATTAAGTCAAGCATCCAGCGACTGAGTGATTCCCTCTTCCCTTTTCGCT 625
Db 636 CCGGACACCGTGTGCAAGGCTGAGCGCTGTGCGACTACCCCGAGTACATGTGTT 695
QY 626 AGCTCTCTTTGTAGAAGAAACGGTTTACACAGGCCAAACTATTAGCTGCTCAGGAATA 685
Db 696 TCTCTGTACTGCGAGGGGACGGCTTACGGAGACCAAGCACCGCGTTAGCATGAGGT 755
QY 686 TGCCACTTCACTGATGCTGTCTCTAGAAATGTTTGTATCCAAAGAACTAAGGCTTT 745
Db 756 GGCGGCTGCTAAGGGCTTCTCTGCTCAAGTACCACTGCTGCGCGGACCAAGGGCTT 815
QY 746 TGTCTTGCAGTAAGTCAATATGCTGCTCATTTGTTCTTCCCTGCTTATGATGTAAACAGTAGC 805
Db 816 CACCACCGCAGTCAAGTGCCTCCGGGGGACAGTCCGAGCTGTCTATGATGTAACCCGTAA 875
QY 806 CATCCCTAAGAGTTCCTCTCTCTCAATGCTAAGACTCTTCAAGGGAACAACCTTCAGT 865
Db 876 CTTCT---AGAGAAACAAAGAACCGCTCTCTGCTGGGATCTCTACGGGAAGAGTACGA 932
QY 866 GGTGATGTTTCAATATCAAGAGGCAATTTGATGAAGAACTGCCAGATACAGATGAGGCTGT 925
Db 933 GCGGACATGCTGCTGAGGAGATTCTCTGGAAGACATCCCGCTGGATGAAAAGGAAGC 992
QY 926 TGCTCAATGTTGCTGAGATATATTGTTGGCCAAAGATGCTTTGTTAGACAAACATATGGC 985
Db 993 AGCTCAGTGGCTTCATAAAGTGTACAGGAGAGGACGGCTCCAGGAGATATATAATCA 1052
QY 986 TGAGGCTACTTTTAGTGTATCAAGAGCTGCAGGATCTGTTGTCGACC 1030
Db 1053 GAAGGCGATGTTTCCAGGGAGCAGTTTAAAGCTTCCCGGAGGCC 1097

RESULT 6

US-09-970-989A-12
; Sequence 12, Application US/09970989A
; Patent No. 6670143
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: ADUREL, DANIEL
; APPLICANT: HOLLENBACK, DAVID
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0275
; CURRENT APPLICATION NUMBER: US/09/970,989A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/215,252
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (184)..(1311)
US-09-970-989A-12

Query Match 8.1%; Score 121.8; DB 4; Length 1660;
Best Local Similarity 46.9%; Pred. No. 6.5e-27;
Matches 415; Conservative 0; Mismatches 467; Indels 3; Gaps 1;
QY 146 CGTGGTGTATCATTTGGCGCTCTCTCTGGCTCCGGCTCTTTGTTAACTCATTC 205

Db 843 CACCACCGCAGTCAAGTGCCTCCGGGGGACAGTCCGAGCTGTCTATGATGAACCTGAA 902
QY 806 CATCCCTAAGAGTTCCTCCTCTCTCAATGCTAAAGACTTTTCAAGGGACCACTTCAGT 865
Db 903 CTC--AGAGGAAACAAGAACCGTCCCTGCTGGGGATCCTCTACGGGAAGATACGA 959
QY 866 GGTGCATGTTTCATCAAGAGGCAATTTGATGAAGGAACGCCAGATACAGATGAGGCTGT 925
Db 960 GGGGACATGTCGTGAGGAGATTCTCTGGAAGACATCCCGCTGGATGAAAGGAAGC 1019
QY 926 TGCTCAATGCTGCGAGATATATTTGGCCCAAGGATGCTTTTGTAGCAAAACATATGCC 985
Db 1020 AGTTCAGTGGCTTCATAACTGTACCAAGGAAGGACGGCTCCAGGAGATATATAATCA 1079
QY 986 TGAGGGTACTTTTAGTGATCAAGAGCTGCAGGATACTGTGTCGACC 1030
Db 1080 GAAGGGCATGTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCC 1124

RESULT 8

US-09-215-252-14
; Sequence 14, Application US/09215252
; Patent No. 630487
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: ADUREL, Daniel
; APPLICANT: HOLLENBACK, David
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0151
; CURRENT APPLICATION NUMBER: US/09/215,252
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1523
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (233)..(1174)
US-09-215-252-14

Query Match 7.2%; Score 108.6; DB 4; Length 1523;

Best Local Similarity 47.6%; Pred. No. 7e-23;
Matches 352; Conservative 0; Mismatches 384; Indels 3; Gaps 1;

QY 292 AGCTTGATGGCTTATTGATTGGTGGCAGAGTTAAGGTCCAAATATTCACAGATCATG 351
Db 225 AACTGGTCATGCTGCTGAGTGGTGTCTGACGAGGTGTACTGTTTCACGGACCAG 284
QY 352 AAACCTTTTCGTTTAAAGGTAAGAGATGCATCTGTGATGAAGCAATCAAGAAGTGATA 411
Db 285 CCACGGTAGAGCGCTTTGGGAAGGAGCAGCAGTGCATCTCTCAACCACTTCGAGA 344
QY 412 TTGATTGGCTTGTGATGGGTTTACGTCAGAGTTCAGGTGTCTTGGCAGACATCTAG 471
Db 345 TCGACTTCTCTGTGGGTGACCATGTGTGAGCGCTTCGAGTGTGGGAGCTCCAAG 404
QY 472 CTGTGATGAAGAAATCTTCAAAGTTTCTGCGGCTCATTTGGCTGGTCAATGTGTTTCG 531
Db 405 TCCTCGCTAAGAAGGAGCTCTCTACGTGCCCTCATCGCTGACGCTGAGCTGTCTTCTG 464
QY 532 AGTATCTTTTTCGGAGAGAGTTGGCCCAAGATGAAGACATTAAGATCAGGATCC 591
Db 465 AGATTGTGTTCTCAAGCGGAAGTGGGAGGAGACCGGACACCGGTGCGAAGGCTGA 524
QY 592 AGGCACTGAGTATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAGGAACCGCTT 651
Db 525 GGGCGCTGTCGGACTACCCCGAGTACATGTGGTTTCTCTGCTACTCGGAGGGACCGCT 584

QY 652 TTACACAGGCCAAACTATTAGTCTCTCAGGAATATGCCACTTCCACTGGATTGCTGTTC 711
Db 585 TCACGGAGACCAAGCACCACCGCTTAGCATGGAGTGGCGGCTGCTAAGGGGCTTCTGTCC 644
QY 712 CTAGAAATGTTTTGATTCCAAGAACTAAGGTTTGTGTCGAGTAAGTCAATATGCGCT 771
Db 645 TCAAGTACCACTGCTGCCGGGACCAAGGCTTTCACACCGCAGTCAAGTGCCTCCGG 704
QY 772 CATTTGTTCTCGCAATTTATGATGTAACAGTAGCATCCCTAAGAGTTCCCTGCTCCTA 831
Db 705 GGACAGTCGAGCTGTCTATGATTAACCTTGAATTC--AGAGGAAACAAGAACCCGT 761
QY 832 CAATGCTAAGACTCTTCAAGGGACAACCTTCAGTGGTGCATGTTTCATATCAAGAGGCAT 891
Db 762 CCTGCTGGGATCCTCTTACGGGAAGAGTACGAGGCGGACATGTGCTGAGGAGATTTC 821
QY 892 TGATGAAGGAAGTCCAGATACAGATGAGGCTGTTGCTCAATGCTGTCGAGATATTTG 951
Db 822 CTCTGGAAGACATCCCGCTGATGAAAGGAGCAGTTCAGTGGCTTCATTAACCTGTACC 881
QY 952 TGGCCAGGATGCTTTTGTAGCAAAACATATGGCTGAGGGTACTTTTAGTGATCAAGAGC 1011
Db 882 AGGAGAAGGACGCGCTCCAGGAGATATATATCAGAGGGCATGTTTCCAGGGGAGCAGT 941
QY 1012 TGCAGGATCTGTGTCGACC 1030
Db 942 TTAAGCTGCCCGGAGGCC 960

RESULT 9

US-09-970-989A-14
; Sequence 14, Application US/09970989A
; Patent No. 6670143
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: ADUREL, DANIEL
; APPLICANT: HOLLENBACK, DAVID
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0275
; CURRENT APPLICATION NUMBER: US/09/970,989A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/215,252
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1523
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (233)..(1174)
US-09-970-989A-14

Query Match 7.2%; Score 108.6; DB 4; Length 1523;

Best Local Similarity 47.6%; Pred. No. 7e-23;
Matches 352; Conservative 0; Mismatches 384; Indels 3; Gaps 1;

QY 292 AGCTTGATGGCTTATTGATTGGTGGCAGAGTTAAGGTCCAAATATTCACAGATCATG 351
Db 225 AACTGGTCATGCTGCTGAGTGGTGTCTGACGAGGTGTACACTGTTTCACGGACCAG 284
QY 352 AAACCTTTTCGTTTAAAGGTAAGAGATGCATCTGTGATGAAGCAATCAGAGAAGTGATA 411
Db 285 CCACGGTAGAGCGCTTTGGGAAGGAGCAGCAGTGCATCTCTCAACCACTTCGAGA 344
QY 412 TTGATTGGCTTGTGAGTGGGTTTTCAGCTCAGCGTTCAGGTGTCTTGGCAGCACTCTAG 471
Db 345 TCGACTTCTCTGTGGGTGGACCATGTGTGAGCGCTTCGGAGTGTCTGGGAGCTCCAAG 404
QY 472 CTGTGATGAAGAAATCTTCAAAGTTTCTGCGGCTCATTTGGCTGTGTCATGTGGTTTCTG 531

Db 405 TCCTCGTAAGAGGAGCTCTCTACGTGCCCCCTCATCGGCTGGACGTGGTACTTTCTGG 464
Qy 532 AGTATCTTTTCTGGAGAGAGTTGGCCCAAGGATGAAGACATTAAGTCAAGCATCC 591
Db 465 AGATTGTGTTCTGCAAGCGGAAGTGGAGGAGACCGGACACCGGTGTCGAAGGGCTGA 524
Qy 592 AGGCACTGAGTATTTCCCTCTTCCCTTTGGTAGCTCTCTTTAGAGGAACCGTT 651
Db 525 GGGCCCTGTCGGACTACCCCGAGTACATGTTGGTTCTCCTGTACTCGAGGGAGCGCT 584
Qy 652 TTACACAGGGCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCCGTTC 711
Db 585 TCAGGAGACCAAGCAGCGGTTAGCATGGAGGTGGCGCTGCTAAGGGCTTCCGTGTC 644
Qy 712 CTAGAAATGTTTGAATCCAAAGTAAAGGTTTGTTCGAGTAAGTCATATGCGCT 771
Db 645 TCAAGTACCACCTGCTGCGCGGACCAAGGGCTTCACCCGAGTCAAGTGCCTCCGG 704
Qy 772 CATTTGTTCTGCCATTATGATGTAAACAGTAGCCATCCCTAAGAGTTCCCTGCTCCTA 831
Db 705 GGACAGTCGAGCTGTATGATGTAAACCTGAACTTC---AGAGAAACAGAACCCGT 761
Qy 832 CAATGTAAAGACTTTCAGAGGACAACTTTCAGTGTGCATGTTTCAATCAAGAGCAT 891
Db 762 CCCTGCTGGGATCCTCTACGGGAAGAAAGTACGAGGGGACATGTCGTGAGGAGATT 821
Qy 892 TGATGAAGGAACTGCCAGATACAGATGAGGCTGTGCTCAATGCTGTCAGATATATTG 951
Db 822 CTCTGGAAGACATCCCGCTGGATGAAGGAAGACAGCTCAGTGGCTTCATTAAGTACC 881
Qy 952 TGCCAAAGTAGCTTTTGTAGCAAAATATGCTGAGGTAAGTCTTTAGTATCAAGAGC 1011
Db 882 AGGAGAGGAGCGCTCCAGGAGATATATCAAGAGGGGATGTTTCCAGGGGAGCA 941
Qy 1012 TGAGGATATGCTGCGACC 1030
Db 942 TTAAGCCTGCCGAGGCC 960

RESULT 10

US-09-215-252-16
; Sequence 16, Application US/09215252
; Patent No. 6300487
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: ADUREL, Daniel
; APPLICANT: HOLLENBACK, David
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0151
; CURRENT APPLICATION NUMBER: US/09/215,252
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1774
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (158)..(1291)
US-09-215-252-16

Query Match 6.7%; Score 100.2; DB 4; Length 1774;
Best Local Similarity 47.0%; Pred. No. 3e-20;
Matches 380; Conservative 0; Mismatches 423; Indels 6; Gaps 2;
Qy 159 TTGGGCTGCTCTCTTCTGCTCCGGCTCTGTTTAAATCTCATTCAGGCAATATCTAT 218
Db 206 TTCTGCTACGCTCTTATGCTCAGGGCTAATCATCAACACCATTCAG---CTCTTCA 262

Qy 219 GTCTGCTAAGCGCGTGTGCAAAAGTTTGTACAGAGGATCAACGGGTAGTAGCAGAG 278
Db 263 CTCCTCTCTGGCCCATTAACAGCAGCTCTTCGGNAGATCAACTGCAGACTGTCTTAT 322
Qy 279 CTCCTTGGCTGGAGCTTGTATGGCTTATTAATGTTGGTGGCAGAGTAAAGTCCAAATA 338
Db 323 TGCATCTCAAGCCAGCTGGTGTATGCTCTGAGTGGTGGTGGGCGACCGAATGCACCAT 382
Qy 339 TTACAGATCATGAACCTTTTCTTAAATGGGTAAAGAGCATCACTTTGTGATAAGCAAT 398
Db 383 TTCAGGACCGCGCGCTTACCTCAAGATAGGAAGAAATGCCATCGTGGTTCTCAAC 442
Qy 399 CACAGAGTATGATTTGATTTGGCTTTGTTGGATGGTTTTCAGCTCAGCGTTTCAGTTGCT 458
Db 443 CACAAGTTTGAATTTGACTTTCTGTGTGGCTGGAGCCTGTCGAAACGCTTTGGGCTGTA 502
Qy 459 GCGAGCTCTAGCTGTGATGAAGAAATCTTCAAGTTTCTGCGGTCATTTGGCTGCTCA 518
Db 503 GGGGCTCCAAAGTCTTGGCCCAAGAAAGAGCTGGCCTATGTCCCAATATTCGGCTGGAT 562
Qy 519 ATGTGGTTTCTGAGTATCTTTTCTGGAGAGAGTTGGGCCCAAGGATGAAGCACATTA 578
Db 563 TGGTACTTCCAGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGATCGCAAGCGTT 622
Qy 579 AAGTCAGGCTCAGGAGCTGAGTATTCCTCTTCCCTTTTGGCTAGCTCTCTTTGTA 638
Db 623 GCCACCAAGTTTGCAGCAGCTCCGGGACTACCCCGAGAAAGTATTTTTCCTGATTCAGT 682
Qy 639 GAAGAACCGGTTTACACAGGCCAACTATTAGCTCTCAGGAATATGCCACTTCCACT 698
Db 683 GAGGCAACAGTTTCCGGAAGACATGAGATCAGATGAGTGGGCCCGGCCAAG 742
Qy 699 GGATTGCTGTTCTTAGAAATGTTTGAATCCAAAGAACTAAGGGTTTGTTCGAGTA 758
Db 743 GGGCTGCTCGCTCAAGCATCACTGTTGCGCAACCAAGGCTTGGCCATCACCGTG 802
Qy 759 AGTCATATGGCTCATTTGTTCTGCGCATTTATGATGTACAGTAGCCATCCCTAAGAT 818
Db 803 AGGAGTTGAGAAATGATGTTTACGCTGTATATGATGCTGATCACTCAATTCAGAAATA 862
Qy 819 TCCCTGCTCTACATGCTAAAGACTCTTCAAGGGACACCTTCAGTGGTGCATGTTTAT 878
Db 863 ---GAAATCCACACTGCTGGAGTCTTAAACGGAAAGAAATACCATGCAGATTGTAT 919
Qy 879 ATCAAGAGGCAATTTGATGAAGAACTCCAGATACAGATGAGGCTGTGTCTCAATGGT 938
Db 920 GTTAGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTCTCGGCTGGCTG 979
Qy 939 CGAGATATTTTGGCCCAAGGATGCTTT 967
Db 980 CACAGCTTACCAGAGAGAGGATGCTTT 1008

RESULT 11

US-09-970-989A-16
; Sequence 16, Application US/09970989A
; Patent No. 6670143
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: ADUREL, Daniel
; APPLICANT: HOLLENBACK, David
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0275
; CURRENT APPLICATION NUMBER: US/09/970,989A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/215,252
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1774

APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1820
; LENGTH: 809
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1820

Query Match 3.4%; Score 51.4; DB 4; Length 809;
Best Local Similarity 47.9%; Pred. No. 1.8e-05;
Matches 148; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 501 CCGGTCTATGGCTGGTCAATGTGGTTTTCTGAGTATCTTTTCTGGAGAGAGTTGGGCC 560
DB 426 CCCACATCCACAGACGACCTACCTTCTGAAATGATTTCCCAAACTGAAGTGGAG 485
QY 561 AAGGATGAAGACATTAAGTACGGATCCAGGATGAGTATTCCTCTTCCCTTT 620
DB 486 GAGGACCGGACACCGGTGTCGAAGGGCTGAGGCGCTGCGGACTACCCCGAGTACATG 545
QY 621 TGGCTAGCTCTCTTTGAGAGGAACGCTTTTACACAGGCCAACTATTAGTGTCTCAG 680
DB 546 TGGTTTCTCTGACTCGGAGGACCGCTTACGAGACCAAGACCCGCTTAGCATG 605
QY 681 GAATATCCACTTCCACTGGATTGCCCTTCTTAGAAGATTTTGTATTCAGAACTAAG 740
DB 606 GAGGTGGGGGTGTAAGGGCTTCTCTCTCAAGTACCACCTGCTGCGCGGACCAAG 665
QY 741 GGTTTTGTCTGAGTAAGTATGAGTATGCTGCTCATTTTCTGCTGCAATTTATGATGAACA 800
DB 666 GGTCTACACCGCAGTCAAGTGCCTCCGGGGACAGTCGAGCTGTCTATGATGTAAACC 725
QY 801 GTAGCCATC 809
DB 726 CTGAACTTC 734

RESULT 13
US-08-213-419B-3/c
; Sequence 3, Application US/08213419B
; Patent No. 6333406
; GENERAL INFORMATION:
; APPLICANT: Inselburg, J. et al.
; TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
; FILE REFERENCE: JII-002CNCIP
; CURRENT APPLICATION NUMBER: US/08/213,419B
; CURRENT FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: US 07/870,506
; PRIOR FILING DATE: 1992-04-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6124
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2407)..(2439)
; NAME/KEY: CDS
; LOCATION: (2598)..(3404)
; NAME/KEY: CDS
; LOCATION: (3580)..(3720)
; NAME/KEY: CDS
; LOCATION: (3850)..(5835)
US-08-213-419B-3

TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (158)..(1291)
US-09-970-989A-16

Query Match 6.7%; Score 100.2; DB 4; Length 1774;
Best Local Similarity 47.0%; Pred. No. 3e-20;
Matches 380; Conservative 0; Mismatches 423; Indels 6; Gaps 2;

QY 159 TTGGGCTGCTCTCTTCCGCTCCGCTCTCTTGTATCTCATTCAGCAATATGCTAT 218
DB 206 TTCTGCTAGCTTTTATTGCTCAGGCTAATCAACACCATTCAG--CTCTTCACT 262
QY 219 GTCTGCTAAGCGGCTGCGAAAGTTGTGACAGAGATCAACCGGGTAGTACAGAG 278
DB 263 CTCTCTCTGCGCCATTAAACAGCAGCTCTTCCGGAAGATCAACTGCAGACTGTCCCTAT 322
QY 279 CTCTGCTGCTGAGCTTGTATGGCTTATTGATTTGTTGGCAGGAGTTAAGTCCAAATA 338
DB 323 TGCATCTCAAGCAGCTGTGTATGCTGTGGAGTGTGTGCGGACGGAATGCACCATC 382
QY 339 TTCACAGATCATGAACCTTTCTGTTTAAATGGTAAAGACATGCACTTGTGTAAGCAAT 398
DB 383 TTCACGACCGCGGCTTACCTCAAGTATGGGAAGAAATGCCATCGTGGTTCTCAAC 442
QY 399 CACAGAAGTATGATTTGCTTGGCTTGTGATGGTTTACGCTCAGGTTTCACTTGTCTT 458
DB 443 CACAAGTTTGAATTTGACTTCTGTGTGCTGGAGCCTGTCGAGACGCTTTGGGTGTGA 502
QY 459 GGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTCCGCTCATTTGGCTGGTCA 518
DB 503 GGGGGCTCCAAAGTCTGCGCAAGAAAGCTGGCTATGTCCCAATATTCGCTGGATG 562
QY 519 ATGTGTTTTCTGAGTATCTTTTCTGGAGAGAAGTTGGGCAAGGATGAAGACATTA 578
DB 563 TGTACTTCCACGAGATGCTTCTGTGCTGGAGCCTGTCGAGACGCTTTCGCAAGCGGT 622
QY 579 AAGTCAGGATCAGCAGCTGAGTATTTCCCTCTTCCCTTTGGTAGCTCTCTTTGTA 638
DB 623 GCCACAGTTTGACGACCTCCGGACTACCCGAGAGATTTTCTGATTCACGTGT 682
QY 639 GAAGAACCGTTTTACAGGCCAAACTATTAGTGTCTCAGGAATATGCCACTTCCACT 698
DB 683 GAGGACACCGGTTCCAGGAGAAGAGCATGAGATCAGCATGCGAGTGGCGCGGCCAAG 742
QY 699 GGATTCCTGTTCTAGAAATGTTTGAATCCAGAACTAAGGTTTGTCTGCACTA 758
DB 743 GGGCTGCTGCTCAGCATCACCTGTTGCCAGAACCAAGGCTTCCCATCCCGTG 802
QY 759 AGTCATATGGCTCATTTGTTCTGCTATTTATGATGATGATGATGATGATGATGATGAT 818
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QY 819 TCCCCTGCTCTCAATGTAAGACTCTTCAAGGGACAACCTTCAGTGTGTGATGTTCTAT 878
DB 863 ---GAAAAATCCAACTGCTGGAGTCTTAAACGGAAAGAAATACCATCAGATTTGTAT 919
QY 879 ATCAAGAGGCAATTTGATGAAGAACTGCCAGATACAGATGAGGCTGTGCTCAATGGTGT 938
DB 920 GTTAGAGGATCCACTGGAGACATCCCTGAGACGATGACGAGTGTGCTGGCTGGCTG 979
QY 939 CGAGATATATTGTGCGCAAGATGCTTT 967
DB 980 CACAAGCTCTACCAGGAGAGGATGCTT 1008

RESULT 12
US-09-833-381-1820
; Sequence 1820, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:

Query Match 3.0%; Score 45.4; DB 4; Length 6124;
Best Local Similarity 48.3%; Pred. No. 0.005;
Matches 127; Conservative 0; Mismatches 136; Indels 0; Gaps 0;
QY 1236 AAGTCAAAAACAGGGCTTCTGATTTATTTGGGAACTTAAAGTTGCAATGATGTA 1295
Db 2324 ATGTTAATAATATGATTTTATAAATATATATATATTTTATTTTATTTT 2265
QY 1296 TGAGTGACTCATGTAATACATTTATTTGCTTTCAACATCTTATCATAGTATGCTTCTA 1355
Db 2264 GGCAATCTAATTTTAAATTTAAATTTAAATTTATATATATATATATATTA 2205
QY 1356 TTCTATATGTAATGTAATGCTTATCGATTCATTTTAAATTTAATTTAGGATA 1415
Db 2204 ATATAAATATATATATTTAAATTTAAATTTTATTTTATTTTATTTTATTTT 2145
QY 1416 TCCTTTTGTATTCACAGCTTAGGGGATGCGCTAGAAAATTCACACCTATTTTATTT 1475
Db 2144 TTTTITTTTTTGACATTTCTAATAGAAATAATCTAGAAATGACCTCTTTTATTTT 2085
QY 1476 AAAAAAATAAAAAAAACT 1498
Db 2084 AATTATCAAAAAAATATATT 2062

RESULT 14

US-08-956-171B-54
; Sequence 54, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13794 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; QUERY MATCH 2.8%; Score 42; DB 1; Length 1562;
; Best Local Similarity 56.5%; Pred. No. 0.022;
; Matches 78; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 1359 TATATATGTAATATGATGCTTATCGATTCATTTTAAATTTAGGATATCC 1418

SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-08-956-171E-54
Query Match 2.8%; Score 42.2; DB 4; Length 13794;
Best Local Similarity 54.1%; Pred. No. 0.086;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 700 GATTGCTGTTCCPAGAAATGTTTGTATCCCAAGAACTAAGGGTTTGTCTTCAGTAA 759
Db 1029 GAGTATCTGCTCCGGAACCTCTTGGACACTATATCTGAGTGCCTGTTCTTCATAA 1088
QY 760 GTCATATGCGCTCATTTTGTTCCTGCCATTTATGATGTAACAGTAGGCATCCCTTAAGATT 819
Db 1089 CGTCAATCAACTGTTTTCACCTGCTGGCACTTCAGATTCAACATATGTCACCTAATAA 1148
QY 820 CCCCTGCTCTACAACTCTAAGACTCTTCAAGGAGCAAC 858
Db 1149 CCGCAATGGTTTCAATCCGATAAATTGACGCGCAGAAC 1187

RESULT 15

US-08-330-108-1
; Sequence 1, Application US/08330108
; Patent No. 5795752
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A.
; TITLE OF INVENTION: IL-2-Stimulated Gene
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,108
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,736
; FILING DATE:
; APPLICATION NUMBER: US/07/796,066
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1562 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: human
; CELL TYPE: T-cell blast
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: 1A8-T7
; US-08-330-108-1
; QUERY MATCH 2.8%; Score 42; DB 1; Length 1562;
; Best Local Similarity 56.5%; Pred. No. 0.022;
; Matches 78; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 1359 TATATATGTAATATGATGCTTATCGATTCATTTTAAATTTAGGATATCC 1418

Db 1408 TATTTATTTATTGTGACAAATGGAGCTGGTTTCTAGATATGATGATGTTTGCAATCCC 1467
Qy 1419 TTTTGTATTGACAGTCTAGGGATGGCCTAGAAAATTCAACCACTATTTTATTTTAAA 1478
Db 1468 CATTTTCTGTTTCAGCATGTTATATCTTATAAATAAAGCAAAGTCAAATATGAAA 1527
Qy 1479 AAAAAAAAAAAAAAAAAA 1496
Db 1528 AAAAAAAAAAAAAAAAAA 1545

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Job time : 99 secs

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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 21:00:33 ; Search time 519 Seconds
(without alignments)
14067.586 Million cell updates/sec

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Perfect score: 1498
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1347.2	89.9	1593	13	US-10-424-599-135471
2	1131	75.5	1394	13	Sequence 10439, A
3	1108.4	74.0	1394	13	Sequence 135449, A
4	1107	73.9	1302	13	Sequence 6209, Ap
5	1017	67.9	1750	13	US-10-425-114-6209
6	866.8	57.9	1583	13	US-10-424-599-67243
7	849.4	56.7	1435	13	Sequence 11471, A
8	842.2	42.9	1515	8	US-10-425-114-9374
9	552.6	36.9	1709	13	US-08-818-581B-3
10	550.8	36.8	1829	17	US-10-425-114-28840
11	549.4	36.7	1550	13	US-10-437-963-27991
12	453.6	30.3	1220	13	US-10-425-114-26574
13	437.6	29.2	1646	13	Sequence 2048, A
14	413.6	27.6	717	13	US-10-425-114-16071
					Sequence 16071, A
					Sequence 135460, A

15	388.8	26.0	581	17	US-10-021-323-14948
16	372.6	24.9	603	17	Sequence 14948, A
17	368.2	24.6	1149	13	US-10-021-323-617
18	366.4	24.5	571	13	Sequence 617, App
19	285.8	19.1	459	13	US-10-425-114-35660
20	233.8	15.6	501	13	Sequence 35660, A
21	150	10.0	279	9	US-10-424-599-51032
22	125	8.3	467	13	Sequence 51032, A
23	121.8	8.1	1660	9	US-10-424-599-123654
24	121.8	8.1	1660	17	Sequence 123654, A
25	121.8	8.1	1660	17	Sequence 87069, A
26	121.8	8.1	1660	17	Sequence 87069, A
27	120.2	8.0	1128	9	US-09-798-029-13
28	120.2	8.0	1769	15	US-10-037-270-841
29	120.2	8.0	1769	16	Sequence 841, App
30	120.2	8.0	1832	9	US-10-117-722-841
31	120.2	8.0	1960	13	Sequence 841, App
32	120.2	8.0	3060	10	US-09-798-029-5
33	120.2	8.0	3060	12	US-09-946-374-296
34	120.2	8.0	3060	13	Sequence 296, App
35	120.2	8.0	3060	13	US-10-015-395A-296
36	120.2	8.0	3060	13	Sequence 337, App
37	120.2	8.0	3060	13	US-10-206-915-337
38	120.2	8.0	3060	13	Sequence 337, App
39	120.2	8.0	3060	13	US-10-199-670-337
40	120.2	8.0	3060	13	Sequence 337, App
41	120.2	8.0	3060	13	US-10-174-581-337
42	120.2	8.0	3060	13	Sequence 337, App
43	120.2	8.0	3060	13	US-10-176-483-337
44	120.2	8.0	3060	13	Sequence 337, App
45	120.2	8.0	3060	13	US-10-176-914-337
					Sequence 337, App
					US-10-176-915-337
					Sequence 337, App
					US-10-006-485A-296
					Sequence 296, App

ALIGNMENTS

RESULT 1
US-10-424-599-135471
; Sequence 135471, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 135471
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_9333C.1
US-10-424-599-135471

Query Match	89.9%	Score	1347.2	DB	13	Length	1593
Best Local Similarity	99.4%	Pred. No.	0				
Matches	1352	Conservative	0	Mismatches	8	Indels	0
Gaps	0						
QY	117	GGCGTGGCATGGCTATTGCACGCGCGGTGGTACCATTTGGGCTGCTCTTTC	176				
Db	225	GGCTGGCCATGGCTATTGCACGCGGTGGTGGTGGCCATTGGGCTGCTCTTTC	284				
QY	177	GGCTCGGCTCCTTGTAACTCTATTGAGCAATATGCTATGCTGTAAGCGCGGTG	236				
Db	285	GGCTCGGCTCCTTGTAACTCTATTGAGCAATATGCTATGCTGTAAGCGCGGTG	344				
QY	237	TGCAAAAGTTGTACAGAGGATCAACCGGGTAGTAGCAGACTTTTGGTGGAGCTT	296				

Db 345 TCAGAAAGTTTGTACAGAAAGATCAACGGGTAGTAGCAGAGCTCTTTGTGGCTGGAGCTT 404
QY 297 GTATGGCTTAATGATTGTGGCGCAGGAGTTAAAGTCCAAATATATTCACAGATCATGAAC 356
Db 405 GTATGGCTTAATGATTGTGGCGCAGGAGTTAAAGTCCAAATATTCACAGATCATGAAC 464
QY 357 TTTGGTTAAATGGGTAAAGAGCATGCACTTGTGATAGCAATCAAGAAAGTGTATTTGAT 416
Db 465 TTTGGTTAAATGGGTAAAGAGCATGCACTTGTGATAGCAATCAAGAAAGTGTATTTGAT 524
QY 417 TGGCTTGTGATGGGTTCAGCTCAGGTTTCAGGTTGTCTTGGCAGCACTCTAGCTGTG 476
Db 525 TGGCTTGTGATGGGTTCAGCTCAGGTTTCAGGTTGTCTTGGCAGCACTCTAGCTGTG 584
QY 477 ATGAAGAAATCTTCAAAAGTTTCTGCCGTCATTTGGCTGGTCAATGTGTTTCTAGTAT 536
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Db 645 CTCTTCTCGAGAGAGTTGGGCCAAGATCAAGCAATTAAGTCAGGCATCCAGCGA 704
QY 597 CTGAGTGAATTCCTCTTCCCTTTGGCTAGCTCTCTTCTAGAAAGCAAGCGGTTTACA 656
Db 705 CTGAGTGAATTCCTCTTCCCTTTGGCTAGCTCTCTTCTAGAAAGCAAGCGGTTTACA 764
QY 657 CAGGCCAAATATAGCTGCTCAGGAATATGCCACTTCCACTGGATGCTGTCTCTAGA 716
Db 765 CAGGCCAAATATAGCTGCTCAGGAATATGCCACTTCCACTGGATGCTGTCTCTAGA 824
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Db 825 AATGTTTTGATTCAGAACTAAGGTTTGTCTTGCAGTAAGTCAATGCGCTCATTT 884
QY 777 GTTCTGCCATTTATGATTAACAGTAGCCATCCCTAAGAGTTTCCCTGCTCTCAATG 836
Db 885 GTTCTGCCATTTATGATTAACAGTAGCCATCCCTAAGAGTTTCCCTGCTCTCAATG 944
QY 837 CTAGACTCTTCAAGGACAACTTCAAGTGTGATGTTTCAATCAAGAGGATTTGATG 896
Db 945 CTAGACTCTTCAAGGACAACTTCAAGTGTGATGTTTCAATCAAGAGGATTTGATG 1004
QY 897 AAGGAACTGCCAGATCAGATGAGGCTTGTCTCAATGTTGTGCGAGATATTTGTGGCC 956
Db 1005 AAGGAACTGCCAGATCAGATGAGGCTTGTCTCAATGTTGTGCGAGATATTTGTGGCC 1064
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Db 1065 AAGGATGCTTTGTAGCAAAATATGCTGAGGTTACTTTAGTGATCAAGAGCTGCG 1124
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Db 1125 GATACCTGGTGCACCAATAAGTCTCTCTGTTAGTTATATCTTGGCGGTGCTGTTGTT 1184
QY 1077 GCGGGTCTGTAAGTTCTCGAAATGGTCTTCTGTTACTCTCTTCTCGGAAGGTTGCA 1136
Db 1185 GCGGGTCTGTAAGTTCTCGAAATGGTCTTCTGTTACTCTCTTCTCGGAAGGTTGCA 1244
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QY 1197 CAGTCAGAGCTTCAAAACCGGCCAAGATCGTCCCTGCAAGTCAAAAACAAAGGGTCT 1256
Db 1305 CAGTCAGAGCTTCAAAACCGGCCAAGATCGTCCCTGCAAGTCAAAAACAAAGGGTCT 1364
QY 1257 TGATTTATTTGGGAACTTAAGTTGCAATTTATGTTGATGATGATCATCTATATCT 1316
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QY 1317 ATTTATTTGCTTTCAACATCTTATCATAGTAGTCTTCTATTTCTATATATGTAATG 1376
Db 1425 ATTTATTTGCTTTCAACATCTTATCATAGTAGTCTTCTATTTCTATATATGTAATG 1484

QY 1377 AATGCTTATCGATTCATTTGTTTAAATTAATAGGATATCCTTTTGTATTGACAGTCTA 1436
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Db 1545 GGGGATGCGCTAGAAAAATTCACCCCTATTTATTTTA 1584

RESULT 2
US-10-425-114-10439
; Sequence 10439, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53)1313B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10439
; LENGTH: 1131
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700909008_FLI
US-10-425-114-10439

Query Match 75.5%; Score 1131; DB 13; Length 1131;
Best Local Similarity 100.0%; Pred. No. 4.8e-287; Mismatches 0; Indels 0; Gaps 0;
Matches 1131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 GCGCGGTGTCGAAAGTTTGTACAGAAAGATCAACCGGTAGTAGCAGAGCTCTTGTGGC 288
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QY 289 TGGAGCTTGTATGCTTATTTGATTGGTGGCAGAGTTAGGTTCCAAATATTCACAGATC 348
Db 61 TGGAGCTTGTATGCTTATTTGATTGGTGGCAGAGTTAGGTTCCAAATATTCACAGATC 120
QY 349 ATGAACCTTTTCGTTTAAATGGTAAAGAGCATGCACTTGTGATAAGCAATCAAGAGTG 408
Db 121 ATGAACCTTTTCGTTTAAATGGTAAAGAGCATGCACTTGTGATAAGCAATCAAGAGTG 180
QY 409 ATATTGATTGGCTTGTGGATGGTTTCAGCTCAGGTTTCAGGTTGCTTGTGGCAGACTC 468
Db 181 ATATTGATTGGCTTGTGGATGGTTTTCAGCTCAGGTTTCAGGTTGCTTGTGGCAGACTC 240
QY 469 TAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCGGTCATTGGCTGCTCAATGTTGTTT 528
Db 241 TAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCGGTCATTGGCTGCTCAATGTTGTTT 300
QY 529 CTGAGTATCTTTTCTGGAGAGAGTTGGGCCAAGAGTGAAGCAATTAAGTCAAGGCA 588
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481 TTCTTAGAAGTGTTCGATCCAAAGAACTAAGGGTTTGTTCGAGTAAGTCAATATGC 540
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841 TGGTGTGCGGGTCTGTAAAGTCTCTGCAATGCTCTGCTGATGTTACTCTTCTGGAAGG 900
1129 GTCTTCGATTTTTCAGCTTTTGGTGTGCGAGTGTGTTACTGCACCTATGCAATTTCTGATTC 1188
901 GTCTTCGATTTTTCAGCTTTTGGTGTGCGAGTGTGTTACTGCACCTATGCAATTTCTGATTC 960
1189 AATTTCTCACAGTCAGAGCGTTTCAACCCGCGCAAGATCGTCTGCAAAAGTCAAAAAACA 1248
961 AATTTCTCACAGTCAGAGCGTTTCAACCCGCGCAAGATCGTCTGCAAAAGTCAAAAAACA 1020
1249 AGGGGTCTGATTTATTTGGCGAATCTTAAAGTGTGATTTATGTTGATGAGTCACTCATG 1308
1021 AGGGGTCTGATTTATTTGGCGAATCTTAAAGTGTGATTTATGTTGATGAGTCACTCATG 1080
1309 TAATCTCATTTATTTGCTTTCAACATCTTATCATAGTATGCTTCTATTTCT 1359
1081 TAATCTCATTTATTTGCTTTCAACATCTTATCATAGTATGCTTCTATTTCT 1131

RESULT 3
US-10-424-599-135449
; Sequence 135449, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 135449
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9331C.1
US-10-424-599-135449

Query Match 74.0%; Score 1108.4; DB 13; Length 1394;
Best Local Similarity 88.0%; Pred. No. 4.9e-281;
Matches 1295; Conservative 0; Mismatches 1; Indels 176; Gaps 1;

QY 5 GAGGTTCGGTTTGTGACCTGACCTCGGAATCCAAAGAGGGAACTCACGGTGTTCGT 64
DB 90 GTGGTTCGGTTTGTGACCTGACCTCGGAATCCAAAGAGGGAACTCACGGTGTTCGT 149
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QY 65 TGGCTTGTCTGTCTGTCTCTTCTTGGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 124
DB 150 TGGCTTGTCTGTCTGTCTCTTCTTGGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 209
QY 125 CATGCTATTGTCAGCAGCGCGGTGGTGTACCAATTTGGGCTGTCTCTTCTTGGCTCCGG 184
DB 210 CATGCTATTGTCAGCAGCGCGGTGGTGTACCAATTTGGGCTGTCTCTTCTTGGCTCCGG 269
QY 185 CCTCTTTGTTAACTCATTCAAGCAATATGCTATGTCTGTAAAGCGCGGTGTGCAAAAG 244
DB 270 CCTCTTTGTTAACTCATTCAAGCAATATGCTATGTCTGTAAAGCGCGGTGTGCAAAAG 329
QY 245 TTTCATCAGAGGATCAACCGGTAGTACAGAGCTCTTGTGGCTGAGCTTGTATGGCT 304
DB 330 TTTCATCAGAGGATCAACCGGTAGTACAGAGCTCTTGTGGCTGAGCTTGTATGGCT 389
QY 305 TATTGATTTGGTGGCAGGAGTTAAGGTTCAAAATATTCACAGATCATGAAACCTTTCTTT 364
DB 390 TATTGATTTGGTGGCAGGAGTTAAGGTTCAAAATATTCACAGATCATGAAACCTTTCTTT 449
QY 365 AATGGGTAAGAGATGACCTTTGTGATAAGCAATCACAGAGTATGATTTGGCTTGT 424
DB 450 AATGGGTAAGAGATGACCTTTGTGATAAGCAATCACAGAGTATGATTTGGCTTGT 509
QY 425 TGGATGGGTTTCACTCAGCTCAGCGTTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAA 484
DB 510 TGGATGGGTTTCACTCAGCTCAGCGTTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAA 569
QY 485 ATCTTCAAAGTTTCTGCGGTCATTGGCTGTCTAATGTGGTCTTCTGAGTATCTTTTCT 544
DB 570 ATCTTCAAAGTTTCTGCGGTCATTGGCTGTCTAATGTGGTCTTCTGAGTATCTTTTCT 629
QY 545 GGAGAGAGTTGGCCCAAGGATGAAGCACATTAAGTTCAGGCACTCCAGCGACTGAGTGA 604
DB 630 GGAGAGAGTTGGCCCAAGGATGAAGCACATTAAGTTCAGGCACTCCAGCGACTGAGTGA 689
QY 605 TTTCCTCTTCCCTTTTGGCTAGCTCTCTTGTAGAAGAACCGGTTTACACAGGCGAA 664
DB 690 TTTCCTCTTCCCTTTTGGCTAGCTCTCTTGTAGAAGAACCGGTTTACACAGGCGAA 749
QY 665 ACTATTAGCTCTCAGGAATATGCCACTTCCACTGGATTCGCTCTTCTAGATGATTTT 724
DB 750 ACTATTAGCTCTCAGGAATATGCCACTTCCACTGGATTCGCTCTTCTAGATGATTTT 809
QY 725 GATTCCAAAGAACTAAGGTTTGTCTTCTGAGTAAGTCAATATGCGCTCATTTGTTCTCTGC 784
DB 810 GATTCCAAAGAACTAAGGTTTGTCTTCTGAGTAAGTCAATATGCGCTCATTTGTTCTCTGC 869
QY 785 CATTTATGATGTAACAGTAGCCATCCCTTAAGAGTTCCCTCTCTCTACATGCTAAGACT 844
DB 870 CATTTATGATGTAACAGTAGCCATCCCTTAAGAGTTCCCTCTCTCTACATGCTAAGACT 929
QY 845 CTTCAGGGACAACTTCCAGTGGTGCATGTTCAATCAAGAGGCAATTTGATGAAGAACT 904
DB 930 CTTCAGGGACAACTTCCAGTGGTGCATGTTCAATCAAGAGGCAATTTGATGAAGAACT 961
QY 905 GCCAGATACAGATGAGGCTGTGTTCAATGTTGCGAGATATATTTGTCGCAAGGATGC 964
DB 962 ----- 961
QY 965 TTTGTTAGCAACAATATGGCTGAGGTTACTTTTAGTGATCAAGAGCTGCAGGATACCTGG 1024
DB 962 ----- 961
QY 1025 TCGACCAATAAAGTCTCTTCTGAGTTATATCTTTGGCGGTGTCTGCTGTTGTCGGGGTC 1084
DB 962 -----ATATCTGGCGGTGTCTGCTGTTGTCGGGGTC 993
QY 1085 TGTAAAGTTCTGCAATGCTTCTGTTACTCTCTTCTCGGAAGGGTGTGATTTTTCAGC 1144
DB 994 TGTAAAGTTCTGCAATGCTTCTGTTACTCTCTTCTCGGAAGGGTGTGATTTTTCAGC 1053
```


RESULT 8
US-08-818-581B-3
Sequence 3, Application US/08818581B
Publication No. US20020007499A1
GENERAL INFORMATION:
APPLICANT: SLABAS, Antoni Ryszard
APPLICANT: BROWN, Adrian Paul
APPLICANT: BROUGH, Claire Louise
APPLICANT: KROON, Johannes Theodorus Maria
TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT
TITLE OF INVENTION: 2-ACYLTRANSFERASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
City: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,581B
FILING DATE: March 14, 1997
PRIOR APPLICATION DATA: WO PCT/GB96/00306
APPLICATION NUMBER: WO PCT/GB96/00306
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: GB 9502468.3
FILING DATE: 09-FEB-1995

[illegible]

Db 631 GATGAGGAGATTAGACCAATTGGCCGCCAGTAAATCATTTGCTGGTGAATTTGTTTGG 572
QY 1062 GCGTGTCTGCTGTTGTTGGGGTCTGTAAAGTCTCTGCAATGGTCTTCTGTTACTCTCTTC 1121
Db 571 TCATGCTCTCTTTATATATGCGCGCTCAAGCTCTTCTATGGACTCAACTCTCTGTGACA 512
QY 1122 TGAAGGGTGTGCAATTTTTCAGCTTTTGGTTTGGCAGTTTGTACTGCACTTATGCAAT 1181
Db 511 TGAAGAGAGTTCGGGTTTACGGCTTTCGCTCGCACTGCTGCGGGTCAATGATGTC 452
QY 1182 CTGATTCATTTCTCACAGTTCAGAGCGTTCAAAACCGGCCAAG 1223
Db 451 TTATCATGTTCTCGCACTCAGAGCGATCGAGTCAGCCCAAG 410

RESULT 11
US-10-425-114-26574
; Sequence 26574, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ-ID NOS: 73128
; SEQ ID NO 26574
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4315-045-D9_FLI
US-10-425-114-26574

Query Match 36.7%; Score 549.4; DB 13; Length 1550;
Best Local Similarity 68.8%; Pred. No. 9.2e-134;
Matches 770; Conservative 0; Mismatches 346; Indels 3; Gaps 1;

QY 105 CTGGCTGGGCTGGGCTGGGCTATTCAGCAGCGCGCTGGTGGTGGTACCAATTTGGGC 164
Db 116 CCGAGATCGGAAGCGGCGCCATCGCCATCCGCTCGTCTCGTCTCCCGCTCGGC 175
QY 165 CTGCTCTTCTTGGCTCGGCTCGGCTCTGTTAAATCTCAATCAGGCAATATGCTATGCTC 224
Db 176 CTCTCTTCTCTCTGCTCGGCTCATCTCAACCAATCCAGGCCATCTCTATTTGTGACA 235
QY 225 GTAAGCGGCTGCGAAAGTTTGTACAGAAGGATCAACCGGCTAGTAGCAGAGCTCTTG 284
Db 236 ATAAGGCCCTTTTCCAGAGCTTGTATCGCCGATCAACAGGTTCTTGGCCGAGCTGCTG 295
QY 285 TGGCTGGAGCTTGTATGGCTTTATTTGATTGGTGGCAGGAGTTAAGGTCCTTGGCAGC 344
Db 296 TGGCTCCAGCTTGTCTGGTGGTGGCTGGTGGGCGGCTTAAGGTACAACTACATCGC 355
QY 345 GATCATGAACCTTTCGTTTAAATGGGTAAAGAGCATGCACTGTGTAAGCAATCACA 404
Db 356 GATGAGGAACCTTACCGATCAATGGGTAAAGAGCATGCACTGTGTAAGCAATCACA 415
QY 405 AGTGATATTTGATTGGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 464
Db 416 AGTGATATTTGATTGGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 475
QY 465 ACTTAGCTGTGATGAAGAAATCTTCAAGTTTCTGGCGGCTCATTTGGCTGGTCAATG 524
Db 476 AGCTCGCTGTGATGAAGAAATCTTCAAGTTTCTGGCGGCTCATTTGGCTGGTCAATG 535
QY 525 TTTTCTGAGTATCTTTTCTGGAGAGAAGTTGGGCGCAAGGATGAAGCAATTAAGTCA 584

; LENGTH: 1829
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRF4530_32632C.1
US-10-437-963-27991

Query Match 36.8%; Score 550.8; DB 17; Length 1829;
Best Local Similarity 68.8%; Pred. No. 4.3e-134;
Matches 772; Conservative 0; Mismatches 347; Indels 3; Gaps 1;

QY 102 GGGCTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 161
Db 1528 GGGCAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1469
QY 162 GGCCTGCTCTTCTTCCGCTCCGCGCTCTTGTATCTCATTCAGCAATATGCTATGTC 221
Db 1468 GGCCTCTCTTCTCTCTCTCCGCGCTCATCATCAGCCCATCCAGCGGCTCTGTTCTC 1409
QY 222 GTCGTAAGCGCGTTCGAAAAGTTGTACAGAAGATCAACCGGGTAGTAGCAGAGCTC 281
Db 1408 TCGATAAGGCGGCTTCTCGAAGAGCTTGTACCGCGGATCAACAGGTTCTTGGCCGAGCTG 1349
QY 282 TTGTGGCTGGAGCTTGTATGGCTTATTTGATTTGGTGGCAGGAGTTAAGTCCAAATATTC 341
Db 1348 CTGTGGCTTCAGCTGCTGGCTTGTGGATTTGGATTTGGTGGCAGGAGTTAAGTACACTGCAT 1289
QY 342 ACAGATCATGAACCTTTCTTTAATGGTAAAGCATGCACTTGTGTATAAGCAATCAC 401
Db 1288 GCTGATGAGAACTTTACAGGCAATGGGGAATGACATGCACTTGTCTATATCAATCAT 1229
QY 402 AGAAGTGATATGATTTGGCTTGTGATGGGTTTACGCTCAGGTTGCTGCTGGC 461
Db 1228 CGGAGCGATATCATTTGGCTTATTTGGTGGATTTTGGCAGCGCTCAGGATGCTCTGGA 1169
QY 462 AGCACTTACGCTGATGAAGAAATCTTCAAGTTTCTGCGGCTCATTTGGCTGGTCAATG 521
Db 1168 AGTACACTGCTGTTAAGAAATCATCGAATTTCTTCCAGTTATGCTGGTCCATG 1109
QY 522 TGTCTTCTGAGTATCTTTTCTGGAGAGAAGTTGGGCGCAAGATGAAGCAATTAAG 581
Db 1108 TGGTTTGCAGATATCTTTTGGAAAGAGCTGGGCAAGGATGAAGAAATTAAGAA 1049
QY 582 TCAGGATCAGGAGCTGAGTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 641
Db 1048 TGGGCTCTCAAGGTTGAAGACTTCCCGAGACCAATTTGGCTAGCCCTTTTGTGAG 989
QY 642 GGAACGCGTTTACACAGGCGCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGA 701
Db 988 GGCACCTGCTTACTCCAGCAAGCTTCTAGCAGCTCAGGAGTATGCTGTTTACAGGCT 929
QY 702 TTGCTGTTCTAGAAATGTTTGTATCCAGAACTAAGGTTTGTCTGCTGAGTAAGT 761
Db 928 TTGCCAGCACCCAGAAATGATTGATTCACGATCAAGAGGATTTGTATCAGCTGTAAT 869
QY 762 CATATGCGCTCATTTGTTCTGCTCATTTATGATGTAAACAGTAGCCATCCCTAAGAGTTCC 821
Db 868 ATTATGGGATTTGTTCCAGCTATTTATGATACACAGTAATTTCCAAAGATTTCA 809
QY 822 CTGCTCTCAATGCTAAGACTTCTCAAGGAGCAACCTTCAGTGGTGCATGTTCAATC 881
Db 808 CCTCAACCAAACTGCTGCGGATTTTGAAGGGCAATCTTCAGTGGTACATGTTCCCATG 749
QY 882 AAGAGGCAATTTGATGAAGGAACTGCCAGATACAGATGAGGCTGTGCTCAATGGTTCGA 941
Db 748 AAACGTCATGCAATGATGAGATGCCAAAGTCAGAGACGATGTTTCAAAATGGTGC 689
QY 942 GATATATTTGGCCAAAGAGTCTTTGTTAGACAAACATATGCTGAGGAGTACTTTAGT 1001
Db 688 GACATCTTTGTAGCAAGAGTGCATTTACTGGATAAGCATTTGGCGAGCAGCACTTT--T 632
QY 1002 GATCAAGAGCTGCAGGATATCTGTCGACCAATTAAGTCTTCTGCTGAGTATATCTTG 1061

Db 536 TTTGAGAGTACCTCTTTTGGAGAGAGCTGGGCCAAGGATGAAAGACACTAAAGTGG 595
Qy 585 GGCAATCCAGGAGCTAGTGAATTCCTCTTTCCCTTTTGGCTAGCTCTCTTTGTAGAGGA 644
Db 596 GGTCTCCAAAGGTTGAAGAGCTTCCCTAGACCAATTTTGGCTAGCTCTTTTGTAGGCT 655
Qy 645 ACGGTTTACACAGGCCAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGATG 704
Db 656 ACTCGCTTTTCTCAGCAAGCTTCTCGCAGCTCAGGAGTATCGGCTTCCCAAGGCTTA 715
Qy 705 CCTGCTTCTAGAAATGTTTGAATCCAAAGAACTAAGGGTTTCTGTCAGTAAGTCAT 764
Db 716 CCAGCTCCTAGAAATGATTAATTCACAGTACCAAGGATTTGTATCTGCCGTAAATTT 775
Qy 765 ATGGGCTCATTTGTTCTGCTGCATTTATGATGTAAAGTATGCTAGTACCCATCCCT 824
Db 776 ATGGGAGATTTGTTCTCAGGCTATTTACGATACAACTGTAAATGCTTCTTAAAGATTC 835
Qy 825 GCTCCTACAATGCTTAAGACTCTTCAAGGGACAACCTTTCAGTGTGTCATGTTCAATCAAG 884
Db 836 CAACCAACATGCTGCGGATTTTGAAGGGCAATCATCAGTGAATATGTCGCGCATGAA 895
Qy 885 AGGCAATTTGATGAAGGAATGCGAGATPACAGATGAGGCTGTTGCTCAATGGTTCGAGAT 944
Db 896 CGTCATGCAATGATGAGATGCGCAAAATCAAGATGATGAGCTTCAAAATGGTGAAGAC 955
Qy 945 ATATTGTCGCAAGGATGCTTTGTTAGCAAAACATATGCTGAGGTAATTTAGTGAT 1004
Db 956 ATTTTGTGCAAGGATGCTTTACTGCAAAACATTTGCAACAGGCACTTT---CGAT 1012
Qy 1005 CAAGAGCTGAGGATACGTGTGACCAATAAAGTCTCTTCTGCTAGTATATATCTTGGGCG 1064
Db 1013 GAGGAGATTAAGACTATCGCGCCGCCAGTGAAATCATCTGCTGTAACCTGTTTGGTGG 1072
Qy 1065 TGCTGCTGTTGCGGGGCTGTAAGATTCCTGCAATGCTCTGTTACTCTCTCTGCTGG 1124
Db 1073 TGCTGCTGTTGTTGTCGATCGAGTCTTCAAGTGAAGCAGCTCTCTATCGACATGG 1132
Qy 1125 AAGGCTGTTGCAATTTGAGTCTTGTGTTGGCAGTTGTTACTGCACTTATGCAAAATCTG 1184
Db 1133 AGAGGAGTGCATTTCACTGCGCAGGATGGCGCTGTCGACAGGGGTCAATGACGCTTC 1192
Qy 1185 ATTCAATTTCAAGCTCAGGCTTCAAACCGGCCAAG 1223
Db 1193 GTCATGTTCTCCAGGCTGAGCGATGAGCTCAGGCCAAG 1231

RESULT 12

US-10-425-114-2048
; Sequence 2048, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2048
; LENGTH: 1220
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700201362_FLI

US-10-425-114-2048

Query Match 30.3%; Score 453.6; DB 13; Length 1220;
Best Local Similarity 70.1%; Pred. No. 1.4e-108;
Matches 639; Conservative 0; Mismatches 269; Indels 4; Gaps 2;
Qy 312 TGGTGGGAGAGGTTAAGGTCCTCAATATTTACAGATCATGAACCTTTCTGTTAATCGGT 371
Db 2 TGGTGGGAGAGGTTAAGGTCCTCAATATTTACAGATCATGAACCTTTACCGATCAATGGGT 61
Qy 372 AAAGAGCATGCACTTGTGATTAAGCAATCACAGAAAGTATATTTGATTTGGTATGG 431
Db 62 AAAGAGCATGCACTTGTGATTAAGCAATCACAGAAAGTATATTTGATTTGGTATGG 121
Qy 432 GTTTTCAGCTCAGGCTTCAAGTGTGCTTGGGAGCACTTAGCTGTGATGAAGAAATCTTCA 491
Db 122 ATATTGGCCCCAGGCTCAGGCTGCTTGGAAAGTACGCTCGCTGTCATGAAGAAAGTCA 181
Qy 492 AAGTTTCTGCGCGCTCAATGGCTGCTCAATGTGGTGTCTTCTGAGTATCTTTTCTGGAGAGA 551
Db 182 AAGTTTCTTCCAGTCAATTTGGCTGCTCAATGTGGTGTCTTTCAGAGTACCTCTTTTGGAGAG 241
Qy 552 AGTTGGGCCAAGGATGAAGCACATTAAGTACGGCATCCAGGCACTGAGTGAATTCCTT 611
Db 242 AGCTGGGCCAAGGATGAAGACACTAAAGTGGGGTCTCCAAAGGTTTGAAGAAAGTCTCCCT 301
Qy 612 CTTCCTCTTTGGCTAGCTCTCTTTGTAGAAGGAACGGGTTTACACAGGCAACATTA 671
Db 302 AGACCAATTTGGCTAGCTCTTTTGTGAGGTAATCTGCTTACTCCAGCAAGCTTCTC 361
Qy 672 GCTGCTCAGGAATATGCCATCTTCCACTGGAATGCTCTTCTGAAAGTGTGTTGATTTCA 731
Db 362 GCAGCTCAGGATATGCGGCTTCCAGGGCTTACAGCTCTCTAGAAATGATTAATTTCA 421
Qy 732 AGAATAAGGTTTGTGTTCTGCAAGTCAATATGCTCTTCTGCTGCTGCTGCTGCTGCT 791
Db 422 CGTACCAAGGATTTGTATCTGCGGTAAGTATTAATGAGATTTTGTTCAGGCAATTTAC 481
Qy 792 GATGTAAAGTACGAGTCCCTTAAGAGTTCCTCTCTCTCAATGTCTTAAGTCTTCTCAAG 851
Db 482 GATCAACTGTAAATAGTTCTTAAAGATTTCCCTCAACCAACAATGCTGCGGATTTTGAAA 541
Qy 852 GGACACCTTCAGTGGTGTGATTTCAATCAAGAGGCAATTTGATGAAGCACTGCCAGAT 911
Db 542 GGGCAATCATCAGTGAATACATGTCGCGATGAAACGCTCATGCAATGATGAGATGCCAAA 601
Qy 912 ACAGATGAGGCTGTTGCTCAATGCTGCGAGATATATTTTGGCCCAAGGATGCTTTGTTA 971
Db 602 TCAGATGATGAGCTTTCAAAAT-GTGTAAAGACATTTTGTGGCAAGGATGCTTACTG 660
Qy 972 GACAAACATATGCTGAGGCTACTTTTAGTGATCAAGAGCTGCGAGTACTGTGCGACCA 1031
Db 661 GACAAACATTTGGCAACAGGCACTTT---CGATGAGGAGATTAGACCTATCGGCCCGCCA 717
Qy 1032 ATAAAGTCTCTTCTGCTAGTATATATCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCT 1091
Db 718 GTGAATCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
Qy 1092 TTCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1151
Db 778 TTCTTCAAGTGGAGCGAGCTCTTATGCAATGAGAGGAGTGGCAATTCATCTGCCGAGG 837
Qy 1152 TTGCACTGTTACTGCACTTATGCAAAATTTCTCATTAATTTCTCAGTCAAGGCTTCA 1211
Db 838 ATGGCGCTGCTGACAGGGCTCATGCACTTCTCATGTTCTTCCAGGCTGAGCGGTG 897
Qy 1212 AACCGGCCAAG 1223
Db 898 AGCTCAGGCCAAG 909

RESULT 13

US-10-425-114-16071
; Sequence 16071, Application US/10425114
; Publication No. US20040034888A1

GENERAL INFORMATION:
; APPLICANT: Liu, Jinedong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 16071
; LENGTH: 1646
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-054-H6_FLI
US-10-425-114-16071

Query Match 29.2%; Score 437.6; DB 13; Length 1646;
Best Local Similarity 69.5%; Pred. No. 2.7e-104;
Matches 623; Conservative 0; Mismatches 269; Indels 4; Gaps 2;

QY 328 AGTCCAAATATTCAGATCATGAAACCTTCGTTTAAATGGTAAGAGCATGCACTTG 387
DB AGGTACAACTACATGCGGATGAGAAACCTTACCGATCAATGGTAAAGAGCATGCACTCG 488

QY 388 TGATAGCATCACAGAAGTATTCATTCGTTGCTTGGATGGGTTTCAGCTCAGCGTT 447
DB TCATATCAATCATCGAAGTATTCATTCGTTGCTTGGATGGGTTTCAGCTCAGCGTT 548

QY 448 CAGGTTGTCTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAATTTCTGCCGCTCA 507
DB CAGGGTGCCCTTGAAGTACGCTCGCTGTATGAAGAAGTATCCCAAGTTCCCTCCAGTCA 608

QY 508 TTGCGTGGTCAATGTGGTTTCTGAGTATCTTTCTGGAGAGAACTTGGGCCAAGGATG 567
DB TTGCGTGGTCAATGTGGTTTCTGAGTATCTTTCTGGAGAGAACTTGGGCCAAGGATG 668

QY 568 AAAGCACATTAAGTTCAGGCACTCAGGCTGAGTATTCCTCTCTCCCTTTTGGCTAG 627
DB AAAGCACATTAAGTTCAGGCTCCTCAAGGTTGAAGACTTCCCTAGACCAATTTGGCTAG 728

QY 628 CTCTTTTGTAGAGGAACGCTTTTACAGGCCAAACTATATAGTGTCTCAGGAATATG 687
DB CTCTTTTGTAGAGGTAATCTGCTTTTACTCCAGCAAAAGCTTCTCGCAGCTCAGGATATG 788

QY 688 CCATTCCTGATTCGCTGTTTCTAGAAATCTTTGATTCAGAACTTAAGGTTTGG 747
DB CGGCTTCCAGGCTTACAGCTTCTAGAAATGATCTTATTCACGTACCAAGGATTTG 848

QY 748 TTTCTGAGTAAGTATATGCGCTCATTTGTTCTGCTCCATTTATGATGTAAACAGTACCA 807
DB TATCTGCGGTAAATATATGCGGATTTTGTTCAGGCAATTTACGATACAACTGTAAATAG 908

QY 808 TCCTTAAGGTTCCCTGCTTCTACATGCTAGACTTCTCAGGCAACCTTCAGTGG 867
DB TTCTTAAGGTTCCCTGCTTCTACATGCTAGACTTCTCAGGCAACCTTCAGTGG 968

QY 868 TGCATGTTCTATATCAAGAGGCAATTTGATGAAGAACTGCGCAGATAGAGCTGTTG 927
DB TACATGTCGCGATGAACGTCATGCAATGATGAGATGCAAAATCAGATGATAC-GTTT 1027

QY 928 CTCATGTTGTCAGATATATTTGTGGCCCAAGATGCTTTGTTAGCAAAACATATGGCTG 987
DB CAAATGTTGTTAAGAGATTTTGTGACAAAGGATGCTTTACTTGGCAAAACATTTGGCAA 1087

QY 988 AGGCTACTTTTAGTCAAGAGCTGCGAGTATCTGCTGACCAATAAAGTCTCTTCTGCG 1047
DB CAGGCACTTT---CGATGAGGAGATTAGACCTTATCGGCCGCCAGCTGAAATCATTTCTCG 1144

QY 1048 TAGTTATATCTTGGCGCTGTCTGTTGTGGGGTCTGTAAAGTCTCTCAATGGTCTT 1107
DB TGACCCCTGTTTGGTCTGCTGCTGTGTTGTTGGTCCATCGAGTCTTCAAGTGGAGCG 1204

QY 1108 CGTTACTCTCTCTCTGAAAGGCTGTTGCAATTTTCAGCTTTTGGTTGGCAGTCTTTACTG 1167
DB AGCTCCTATCAGATGAGAGGAGTGGCAATTCATGCGCAGGAGTGGCGTCTGTGACAG 1264

QY 1168 CACTTATGCAAAATCTGATTCATTCACAGTCCAGAGCTTCAAAACCGGSCCAAG 1223
DB GGGTCATGCGAGCTCTTCTGTCATGTTCTCCAGGCTGAGCGATCGAGCTCAGCCAG 1320

RESULT 14
US-10-424-599-135460
; Sequence 135460, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 135460
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9332C.1
US-10-424-599-135460

Query Match 27.6%; Score 413.6; DB 13; Length 717;
Best Local Similarity 80.0%; Pred. No. 3.4e-98;
Matches 568; Conservative 0; Mismatches 44; Indels 98; Gaps 3;

QY 881 CAAGAGGCAATTTGATGAAGAACTGCCAGATACAGATGAGGCTGTGCTCAATGGTGTG 940
DB CAAGAGGCAATTTAATGAAGAAATTTGCCAGAAACAGATGAGGCTGTGCTCAATGGTGTG 60

QY 941 AGATATATTTGGCCAGGATGCTTTGTTAGCAAAACATATGCTGAGGTAATTTAG 1000
DB AGATATATTTGGCCAGGATGCTTTGTTAGCAAAACATATATAGTGAAGTCTTCTTCTT 120

QY 1001 TGATCAAGAGCTGAGGATATCTGCTCGACCAATAAAGTCTCTTCTGGTAGTATATCTTG 1060
DB TGATCAAGATTTGAGGATATCTGCTCGACCAATAAAGTCTCTTCTGGTAGTATATCTTG 180

QY 1061 GCGGTGCTGTTGTTGGGGGTCTGTAAGTTCCTGCAATGCTGCTGCTGCTCTCTCTTC 1120
DB GGTGTTGCTGTTGTTGGGGGTCTGTAAGTTCCTGCAACGCTCTTCTGCTCTCTCTTC 240

QY 1121 CTGGAAGGCTGTGCAATTTTCAGCTTTTGGTTTGGCAGTCTTCTGCACTTATGCAAT 1180
DB CTGGAAGGCTGTGCAATTTTCAGCTTTTGGTTTGGCAGTCTTCTGCACTTATGCAAT 300

QY 1181 TCTGATCAATTTCTCAGCTCAGAGCGTTCAAAACCGGCCAAGATCGCTGCTGCAAGTC 1240
DB TCTGATCAATTTCTCAGCTCAGAGCGTTCAAAACCGCTGCCAAGATCGCCCGGCAAGTC 360

QY 1241 AAAAACAAGGGG----- 1253
DB AAAAACAAGGGG----- 420

QY 1254 -----TCTTGATTTATT 1265
DB GATTTCCAGAGCCCAAAAGTTTCTATACAAAGATAGGCTTCTCATCTACGATCATATTT 480

QY 1266 TGGGAACTTAAAGTTCATTTATGTGTGATGAGTCACTGTAATTAATCAATATTTTG 1325

Db 481 TGGCGAACTTAAAGTTCATTTATGTGTGATGAGTGACTCATGTAATGCTCATTTATTTTG 540
Qy 1326 CTTTCAACATCTTATCATAGTATGCTTCTATTCTATATATGTAATGCTTAT 1385
Db 541 CTTTCAAAATCTTATCATGATGATGTTCTATTCTATATATGTAATGCTTAT 600
Qy 1386 CGATTCTATGTTTAAATTAATTAAGGATATCCTTTTGTATTGACAGTCTTAGGGGATGGC 1445
Db 601 CGATTCTATGTTTAAATTAATTAAGGATAT-CTTTTGTATGACAACTCTA--GGATGGC 657
Qy 1446 CTAGAAAAATCAACCACTTATTTTATTTAAAAAATAAAAAAAAAAAAAA 1495
Db 658 CTAGAAAAATCAACCGCTCTTTTATTTTAAAAAATAAAAAAAAAAAAAA 707

RESULT 15

US-10-021-323-14948
; Sequence 14948, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021.323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 14948
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-018-Q6-K6-F2
US-10-021-323-14948

Query Match 26.0%; Score 388.8; DB 17; Length 581;
Best Local Similarity 80.5%; Pred. No. 1e-91;
Matches 467; Conservative 0; Mismatches 112; Indels 1; Gaps 1;
Qy 375 GAGCATGCATTTGTGATAACCAATCAAGAGTGAATTTGATGGCTTTGGATGGGTT 434
Db 2 GAACATGCCCTTCTCTTACCCAATCACAG-AGTGATATTGATTGGTTAGTTGGATGGGTT 60
Qy 435 TCAGCTCAGCGTTTCAGGTGTCTTGGCAGACCTAGCTGTGATGAAGAAATCTTCAAAG 494
Db 61 CTGCTCAGCGATCAGGTGTCTTGGCAGTTCAATAGCTGTGATGAAGAAATCAACAA 120
Qy 495 TTCTGCCGCTCATTTGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAGAGT 554
Db 121 TTCTCCCGCTCATAGGTGGTCAATGTGGTTTCTGAGTATCTGTTTTTGGAAACGAAGC 180
Qy 555 TGGGCCAAGGATGAAGACCAATTAAGTCAAGCATCCAGCATGAGTGAATTTCCCTCTT 614
Db 181 TGGGCCAAGGATGAAGACCAATTAAGGATGAAGCATCCAGCTTTAAGGACTATCCACAG 240
Qy 615 CCCTTTGGCTAGCTCTCTTTGTAGAGGAACCGGTTTTACAGGCCAAACTATTTAGCT 674
Db 241 CCATTTGGTTGGCGCTTTTGTAGAGGAACCTCGCTTTTACACAGCAAGGCTTGTGCA 300
Qy 675 GCTCAGGAATATGCCACTTCCACTGATTCCTGTGTTCTAGAAATGTTTGTATTCACAG 734
Db 301 GCTCAGGAATATGCCACTTCCAGGATTCCTATACCTAGAAACGTTTGTATTCCTCGT 360
Qy 735 ACTAAGGGTTTCTTTCTGAGTATGATGCGTCAATTTGTTCTGCCATTTATGAT 794
Db 361 ACAAGGGTTTCTTTCTGAGTATGATGCGTCAATTTGTTCTGCCATTTATGAT 420

Qy 795 GTACAGTAGCCATCCCTAAGAGTTCCCTGCTCTCTACAAATGCTAAGACTCTTCAAGGGA 854
Db 421 ATTACAGTGGCTATTCCCAAAAGCTCACCTTCACTTCAATGCTTAGACTTTTCAAGGGG 480
Qy 855 CAACCTTCAGTGGTGGCATGTTTCATATCAAGAGGCAATTTGATGAAGGAACTGCCAGATACA 914
Db 481 CAATCTTCTGTGTACACGTACATATCAAAAGCACACCTCATGAAGGAACTGCCCTGAAATG 540
Qy 915 GATGAGGCTGTGCTCAATGCTGCGAGATATATTGTTGG 954
Db 541 GATGAGGCTGTGCTCAATGCTGCGAGATATGTTGTTGG 580

Search completed: July 9, 2004, 23:03:53
Job time : 526 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 18:57:17 ; Search time 2827 Seconds
(without alignments)
15823.681 Million cell updates/sec

Title: US-09-914-098-55

Perfect score: 1498

Sequence: 1 gcacgaggttcggttgcgtg.....aaaaaaaaaaaaaact 1498

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pig:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602	40.2	602	14	CA819096 sau68h05.
2	561	37.4	739	13	BQ123121 EST608697
3	533.4	35.6	570	12	BI974194 sai197903.
4	531.8	35.5	824	12	BG585493 EST487257

5	522.8	34.9	1592	11	AY109624	AY109624	Zea mays
6	492.6	32.9	780	12	BG585566	EST487330	
7	485.8	32.4	739	12	CK240532	VRJ34317	
8	476.8	31.8	763	12	BG585567	EST487331	
9	468	31.2	564	12	BM523947	sai105e03.	
10	465.4	31.1	620	10	AW508939	si38b11.y	
11	463.2	30.9	692	14	CA900082	PCSC21606	
12	461.2	30.8	656	10	AW695931	NF100G06S	
13	442.8	29.6	466	14	CD400176	GM_CK2194	
14	436.4	29.1	670	14	CB970126	CAB10003	
15	434.4	29.0	685	13	CF403131	GA_ED005	
16	432.4	28.9	698	14	CF210882	CAB20007	
17	429.6	28.7	649	10	AW773846	EST332832	
18	427.4	28.5	882	10	BF286651	GA_EB000	
19	418.8	28.0	814	14	CD820693	BN20.0531	
20	415.6	27.7	557	14	CA936841	sav25c01.	
21	413.4	27.6	763	14	CF672320	RTCNT1.62	
22	405.6	27.1	564	12	BM892810	sam64f01.	
23	401.2	26.8	746	14	CD836813	BN45.049P	
24	400	26.7	672	14	CB074283	EST070795	
25	399.2	26.6	745	14	CF437515	EST673860	
26	395.6	26.4	490	10	AW620973	sj38e03.y	
27	389.8	26.0	542	14	CA785831	sat39h01.	
28	387.2	25.8	676	14	CD826229	BN25.063C	
29	381	25.4	829	14	CB654545	OSJNE07C	
30	381	25.4	850	14	CB644085	OSJNE05C	
31	377.6	25.2	666	14	CD820168	BN20.051G	
32	371.6	24.8	498	10	BF637273	NP047B10L	
33	370.8	24.8	560	12	BI405683	04BD08.Ma	
34	370.8	24.8	667	14	CD831577	BN40.060B	
35	370.2	24.7	840	14	CB620801	OS1IEA06D	
36	369	24.6	701	12	BJ463828	BJ463828	
37	367.8	24.6	545	14	CA900078	PCSC09348	
38	367.8	24.6	833	14	CB644127	OSJNE05D	
39	367.4	24.5	695	13	BQ764802	EBca01.SQ	
40	365.4	24.4	765	14	CD437887	EL01N0506	
41	365.4	24.4	866	14	CK152069	FGAS03496	
42	360.2	24.0	397	12	BM308598	sak48b08.	
43	359	24.0	636	13	BU879456	V060D12.P	
44	354.2	23.6	776	14	CB682848	OSJNEf10J	
45	351.2	23.4	614	12	BG356169	EM1_22_C1	

ALIGNMENTS

RESULT 1	CA819096	602 bp	mRNA	linear	EST 09-DEC-2002
LOCUS	CA819096	saue68h05.y1	Gm-cl071	Glycine max cDNA clone	SOYBEAN CLONE ID:
DEFINITION	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE. 1, mRNA sequence.	saue68h05.y1 Gm-cl071 Glycine max cDNA clone	Q9SDN3		
ACCESSION	CA819096	GI:26268033			
VERSION	EST.				
KEYWORDS	Glycine max (soybean)				
SOURCE	Glycine max (soybean)				
ORGANISM	Glycine max (soybean)				
REFERENCE	1 (bases 1 to 602)				
AUTHORS	Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.				
	Public Soybean EST Project				
	Unpublished (1999)				
	Contact: Shoemaker R/Public Soybean EST Project				
	Public Soybean EST Project				
	Washington University School of Medicine				

Qy	1201	CAGAGCGTTCAAACCGCGCCACAGATCGTGCTCCAAAGTCAAAAACAGGGGCTTTGAT	1261
Db	481	CAGAGCGTTCAAACCGCGCCACAGATCGTGCTCCAAAGTCAAAAACAGGGGCTTTGAT	540
Qy	1261	TTATTTGGCGAACTTAAAGTTGCATTTATGTGTGATGAGTGACTCATGTAAATACTCAATTA	1320
Db	541	TTATTTGGCGAACTTAAAGTTGCATTTATGTGTGATGAGTGACTCATGTAAATACTCAATTA	600
Qy	1321	TT 1322	
Db	601	TT 602	

Db	601 TT 602
RESULT 2	
LOCUS	BQ123121
DEFINITION	739 bp mRNA linear EST 17-APR-2002 EST608697 GLSD Medicago truncatula CDNA clone pGLSD-31M13, mRNA
ACCESSION	BQ123121
VERSION	BQ123121
KEYWORDS	BQ123121.1 GI:20175083
SOURCE	EST.
ORGANISM	Medicago truncatula (barrel medic)
REFERENCE	Medicago truncatula
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; 1 (bases 1 to 739)
TITLE	Grusak, M.A., Samac, D., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
JOURNAL	ESTs from late stage developing seeds of Medicago truncatula Unpublished (2002)
COMMENT	Contact: Grusak, M.A. USDA/ARS Children's Nutrition Research Center Baylor College of Medicine 1100 Bates Street, Houston, TX 77030-2600, USA Tel: 713 798 7044 Fax: 713 798 7078 Email: mgrusak@bcm.tmc.edu TIGR sequence name: MTRAM797K More information is available at:

1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713 798 7044
Fax: 713 798 7078
Email: mgrusak@bcm.tmc.edu
TIGR sequence name: MTRAM797K More information is available at:
www.medicago.org
Seq primer: SKm0d (CTA GAA CTA gtg GAT CC).
Location/Qualifiers
1. .739
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="Al7"
/db_xref="taxon:3880"
/clone="pGLSD-31M13"
/tissue_type="Immature seeds"
/dev_stage="25 to 35 days after pollination"
/lab_host="XL0LR"
/clone_lib="GLSP"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Immature seeds, collected from pods ranging in age from 25 to 35 days after pollination, were harvested from greenhouse-grown plants. Seed were removed and separated from pod walls and immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the UniZap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

ORIGIN
Query Match 37.4%; Score 561; DB 13; Length 739;
Best Local Similarity 86.5%; Pred. No. 1.4e-86;
Matches 643; Conservative 0; Mismatches 95; Indels 5; Gaps 2;
Qy 409 ATATTGATTCGGTGTGGATGGGTTTCAGCTCAGCTTCAGTTCCTTGGCAGACTC 468

Db	1	ACATTGATGGCTTTTCGGATGGATTTT	AGCTCAGCGTT	CAGGATGCTTGGTAGCAGCG	60
Qy	469	TAGCTGTG - ATGAAGAAATCTTCAAGT	TTTCTGCCGTCATTTGGCTGGTCAATGTGGTTT	527	
Db	61	TTGCTGTGATGAAGAAATCATCTAAGT	TTTCTGCCGTCATTTGGTGGTCAATGTGGTTT	120	
Qy	528	TCTCAGTATCTTTTCTTGGAGAGAGT	TGGGCCAAGNTGAAGCATTAAAGTCAAGC	587	
Db	121	TCTGAATATCTTTCTTGGAGAGAAAT	TGGCCCAAGGATGAAGAACATTAA - - - - AGGC	176	
Qy	588	ATCCAGCGACTGAGTGAATTTCCCTCT	TTCCCTTTTGGCTAGCTCTCTTTGTAGAGGAACG	647	
Db	177	CTACAGCAACTGCGGGATTTCCCTCT	TTCCCTTTTGGCTAGCTCTCTTTGTAGAGGAAC	236	
Qy	648	CGTTTTACAGGCCAACTATTAGCTGCT	CAGGAATATGCCACTTCCACTGGATTGGCT	707	
Db	237	CGCTTTACAGGCCAAATTTATTAGCGCT	CAGGAATATGCAACTCAACTGGATTGGCT	296	
Qy	708	GTTCCTAGAAATGTTTTGATTTCCAAG	AACTAAGGGTTTTGTTCTGCAGTAAGTCATATG	767	
Db	297	GTTCCTAGAAACGTTTTGATTTCCAAG	AACTAAGGGTTTTGTTCTGCAGTAAGTCATATG	356	
Qy	768	CGCTCATTTGTTCTGCGCATTTATGAT	GTAACTAGCTAGCATCCCTAGAGTTCCCTGTCT	827	
Db	357	CGCTCATTTGTTCCAGGCAATTTATG	ATGTATCACTGGTGCATTTCCAGAGTTCCACCCCT	416	
Qy	828	CCTACAAATGCTAAGACTCTTCAAGG	GAACAACCTTCAGTGGTGCATTTTCATATCAAGAGG	887	
Db	417	CCTACAAATGCTAAGACTCTTCAAGG	GAACAACCTTCAGTGGTGCATTTTCATATCAAGAGG	476	
Qy	888	CATTTGATGAAGAACTGCCAGATAC	AGATGAGGCTGTTGCTCAATGGTGTGAGATATA	947	
Db	477	CATTTGATGAAGAAATTTGCCAGAG	CAGAGAGAGCTGTGCTCAATGGTGTGAGAGATATA	536	
Qy	948	TTTGTGCCAAGGATGCTTTGTTTGA	CAAAACATATGGCTGAGGTCATTTTGTAGTGATCAA	1007	
Db	537	TTTGTGCTTAAGATGCTTTGTTTGA	CAACATATCTGCTGATGACAAATTCAGTGATCAC	596	
Qy	1008	GAGCTGCAGGATATCGGTGCAACCA	ATAAAGTCTCTTCTGGTGTAGTTATATCTTGGCGGTGT	1067	
Db	597	GAGCACGGGATCTTGTGCGACCAAT	AAAGTCTCTTCTGGTGTGTCATAAACAATGGAATTTGT	656	
Qy	1068	CTGTTGTTGCGGGTCTGTAAAGTTC	TGCAATGGTCTTCGTTTACTCTCTTCTCTGGAAG	1127	
Db	657	GTGTCGTTGCGGGGACTGTTAAGT	TGCTTCAATGGTCTTCACTACTATCTCTCTGGAG	716	
Qy	1128	GGTTGCAATTTTCAGCTTTTGG	1150		
Db	717	GGTGTGCAATTTTCAGTATTTAG	739		

[illegible]

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
B1974194.1				
B1974194.1	GI:16348599		Glycine max (soybean)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Fabales; Fabaceae; Papilionoideae; Phaseolaceae; Glycine; euredoids 1; Phaseolus 1 to 570)

REFERENCE

1. (Bases 1 to 570)

AUTHORS

Schoemaker, R., Keim, P., Vodkin, L., Expelding, J., Corryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
Cayre, J.

McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 422.

FEATURES	SOURCE
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FEATURES
source
Location/Qualifiers
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/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-9125"
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/lab_host="DH10B"
/clone_lib="Gm-cl065"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Williams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(GT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."

```

ORIGIN

Query Match	35.6%	Score 533.4	DB 12	Length 570
Best Local Similarity	99.8%	Pred. No. 8.7e-92		
Matches 534	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy	5	GAGGTTCCGTTTGCTGCTGACCTGACCTCGGAAATCCAAAGAGGGAACATCACGGTGTTCGT	64	
Db	36	GTGTTCCGTTTGCTGACCTGACCTCGGAAATCCAAAGAGGGAACATCACGGTGTTCGT	95	
Qy	65	TGGTGTGCTGCTGCTGCTGCTCTTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	124	
Db	96	TGGTGTGCTGCTGCTGCTCTCTTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	155	
Qy	125	CATGGCTATTGCAGCAGCGCCGTGTGTGATCCATTGGGCTGCTCTTTTCGCCCTCCGG	184	
Db	156	CATGGCTATTGCAGCAGCGCCGTGTGTGATCCATTGGGCTGCTCTTTTCGCCCTCCGG	215	
Qy	185	CCCTCTGTTAAATCTCATTCAGGCAATATGCTATGCTGCTGAAGGCCGTGTGCGAAAG	244	
Db	216	CCCTCTGTTAAATCTCATTCAGGCAATATGCTATGCTGCTGAAGGCCGTGTGCGAAAG	275	
Qy	245	TTGTGACAGAAGGATCAACCGGTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGTATGGCT	304	
Db	276	TTTGTACAGAAGGATCAACCGGTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGTATGGCT	335	
Qy	305	TATTGATTGTGGCGAGGAGTTAAGGTCCTCAATATTCACAGATCATGAACCTTTGGTTT	364	
Db	336	TATTGATTGTGGCGAGGAGTTAAGGTCCTCAATATTCACAGATCATGAACCTTTGGTTT	395	
Qy	365	AATGGGTAAAGCAGATGCATTTGTGATAAGCAATCAGAGAGTGATATTGATTGGCTTGT	424	
Db	396	AATGGGTAAAGCAGATGCATTTGTGATAAGCAATCAGAGAGTGATATTGATTGGCTTGT	455	
Qy	425	TGGATGGGTTTCAGCTCAGCGTTTCAGTGTGCTTTGGCAGCACTCTAGCTGTGATGAAGAA	484	

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Db      456 TGGATGGGTTTCAAGCTCAGCGTTACAGTTGCTCTTTGGCAGACACTCTCTAGCTGTGATGAAGAA 515
Qy      485 ATCTTCAAAGTTTCTGCGGCTCATTTGGCTGGTCAATGCTGTTTCTGAGTATCTTT 539
Db      516 ATCTTCAAAGTTTCTGCGGCTCATTTGGCTGGTCAATGCTGTTTCTGAGTATCTTT 570

RESULT 4
BG585493
LOCUS   BG585493                824 bp    mRNA    linear    EST 11-APR-2001
DEFINITION   EST487257 MHAM Medicago truncatula/Glomus versiforme mixed EST
              library cDNA clone pHEAM-3019 5' end, mRNA sequence.
ACCESSION   BG585493
VERSION     BG585493.1 GI:13600557
KEYWORDS
SOURCE      Medicago truncatula/Glomus versiforme mixed EST library
ORGANISM    Eukaryota; mixed EST libraries.
REFERENCE   1 (bases 1 to 824)
AUTHORS     Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
            and Fraser,C.M.
TITLE       ESTs from roots of Medicago truncatula after colonization with
            Glomus versiforme, 2001
JOURNAL     Unpublished (2001)
COMMENT     Contact: Harrison M.J.
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73401
            Tel: 580-223-5810
            Fax: 580-221-7380
            Email: mjharrison@noble.org
            Noble EST name: N380967e TIGR sequence name: MTDCE53TK More
            information is available at: http://www.medicago.org
            Seq primer: SKmed (CTA gAA CTA gTG GAT CC).
            Location/Qualifiers
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            /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
            post-inoculation with Glomus versiforme. The library was
            made from a mixture of RNA from each of these stages."
            /lab_host="E. coli strain XL0LR"
            /clone_lib="MHAM"
            /notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
            XhoI; cDNA was prepared from polyA+ enriched RNA from
            roots harvested at 10, 17, 22, 31 and 38 days
            post-inoculation with Glomus versiforme. The cDNA was
            directionally ligated into the Unizap XR vector from
            Stratagene and packaged using Gigapack III Gold packaging
            extracts. Plasmids containing cDNA inserts were excised
            from the recombinant lambda-Zap phage using Ex-assist
            helper phage and propagated in XL0LR cells."

ORIGIN
Query Match          35.5%; Score 531.8; DB 12; Length 824;
Best Local Similarity 87.1%; Pred. No. 1.4e-81;
Matches 595; Conservative 0; Mismatches 87; Indels 1; Gaps 1;

Qy      108 GGTGGCTGGCTGGCATGGTATTCAGACAGCGCGCGTGGTGTACATTTGGCGCTG 167
Db      142 GACAGAGAGAGGCGGCATGGTATTCAGACAGCGCTGCTGTCTGCTGCTCCACTAGCGCTG 201
Qy      168 CTCTTCTCGCCCTCCGCGCTCCTTTGTAATCTCATTCAGGCAATATGCTATGCTGCTGA 227
Db      202 CTCTTCTCGCTCCGCGCTCATGCTTTAATCTTTTCAGGCAATATGCTATGCTGCTAGTA 261
Qy      228 AGCCCGGTGTGAAAAGTTTGTATCAGAAGATCAACCGGTTAGTACAGAGCTCTTTGG 287

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Db      262 AGACCGCTGTCAAAGAAATTTGTACAGAAGGATCAACCGGGTGTGGCAGAACTGTTGTGG 321
Qy      288 CTGAGAGCTTTGTATGGCTTATTGATTGGTGGCGAGGAGTTAAGGTCCAAATATTACAGAT 347
Db      322 CTGGAACCTTTGTTGGCTTATTGATTGGTGGCGTGGAGTTAAGGTGAAATATACCGGAC 381
Qy      348 CATGAAACCTTTGTTTAAATGGGTAAAGACATGCACTTGTGATAAGCAATCAAGAAGT 407
Db      382 CGTGAAACCTTTCTCGTTTGGTGGGTAAAGAACATGCACTTGTATATGCAATCAAGAAGT 441
Qy      408 GATATTGATTGGCTTTGTTGGATGGTTCAGCTCAGCGTTTCAGGTTTGTCTTGGCAGCACT 467
Db      442 GATATTGATTGGCTTTGTTGGATGGTTCAGCTCAGCGTTTCAGGTTTGTCTTGGCAGCACT 501
Qy      468 CTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCGCGGTCAATTTGGTGGTCAATTTGGTTT 527
Db      502 CTAGCAGTGATGAAGAAATCTTCAAAGTTTCTTACCGGTAAATTTGGTGGTCAATTTGGTTT 561
Qy      528 TCTCAGTATCTTTTCTGAGAGAGAGTTGGGCCAAGGATGAAAGCACATTAAAGTTCAGGC 587
Db      562 TCTCAGTATCTTTTCTGAGAGAGAGTTGGGCCAAGGATGAAAGCACATTAAAGTTCAGGC 621
Qy      588 AT-CCAGCGACTGAGTCAATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTTGAAGGAAC 646
Db      622 ATACCGGCGGTTGAATGATTTCCCTCTTCCATTTTGGTGGTCTCTCTTTTGAAGGAAC 681
Qy      647 CGCTTTTACACAGCCCAACTATTAGCTGCTCAGGATATGCCACTTCCACTGGATTGCC 706
Db      682 ACGTTTTCACAAATGTCAAATTTATTTAGCTGCTCAGGAAATGCAACCTCCACTGGATTGCC 741
Qy      707 TGTTCCTAGAAATGTTTGTATTCACAGAACTAAGGGTTTGTCTGTCAGTAAAGTCAATAT 766
Db      742 TGTTCCTAGAAATGCTTGTATTCCTAGACTAAGGGGTTTGTCTGCTGTAAGTCAATAT 801
Qy      767 CGGCTCATTTGTTCTCTGCCATTTT 789
Db      802 CGCATCATTTGTTCTCTGCCGTTT 824

RESULT 5
AX109624
LOCUS   AX109624                1592 bp    mRNA    linear    HTC 17-OCT-2002
DEFINITION   Zea mays CL2286_1 mRNA sequence.
ACCESSION   AX109624
VERSION     AX109624.1 GI:21213416
KEYWORDS    HTC.
SOURCE      Zea mays
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 1592)
AUTHORS     Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE       Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
JOURNAL     Unpublished (2002)
REFERENCE   2 (bases 1 to 1592)
AUTHORS     Coe,E.H.
TITLE       Direct Submission
JOURNAL     Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri-Columbia, MO 65211, USA
COMMENT     If you are interested in getting corresponding physical clones,
            searching at MSU, maizegap.org; zmdB, www.zmdB.iastate.edu; TIGR,
            www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
            maize cDNA sequences is either Virginia Walbot, Stanford or Pat
            Schnable, Iowa State, then clones may be requested from ZmDB:
            www.zmdB.iastate.edu.
            Location/Qualifiers
FEATURES
    source
        1..1592
            /organism="Zea mays"
            /mol_type="mRNA"

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/db_xref="MaizeDB:630905"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN
Query Match          34.9%; Score 522.8; DB 11; Length 1592;
Best Local Similarity 65.7%; Pred. No. 3.6e-80;
Matches 720; Conservative 0; Mismatches 373; Indels 3; Gaps 1;

QY 128 GGCATTTCAGCAGCGCCGCTGGTGTACCAATGGGCTGCTCTTCTTCGCTCCGCGCT 187
DB 214 GGCATCCCGCTCGTGTCTGTGTCTCGCTCGCTCGCTCGCTCTCTCTCTCTGCGGCT 273
QY 188 CCTGTGTAATCTCATTCAGGCAATATGCTATGTCGTCGTAAGCCGCTGTCGAAAGTTT 247
DB 274 CATCGTCAACACATCCAGGCCATCCCTATTGTGTGACAATAAGGCCCTTTTCCAGAGCTT 333
QY 248 GTACAGAAGGATCAACCGGGTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGATGGCTTAT 307
DB 334 GTATCGCGGATCAACACAGGTTCTTGGCCGAGCTGTGGCTCAGCTTGTCTGGGTGT 393
QY 308 TGATTGGTGGCAGGAGTTAAGTCCAAATATTTCAGATCATGAACCTTCGTTTAAAT 367
DB 394 GGAAGTGGTGGCAGGCTTAAAGTACAACCTGCATGCGGATGAGAACTTACCGATCAAT 453
QY 368 GGGTAAAGACATGCACTTGTGTAAGCAATACAGAAGTGATATTGATTGGCTTCTGG 427
DB 454 GGGTAAAGACATGCGCTCTGTCATATCAATCATCAAGTATATTGATTGGCTTATGG 513
QY 428 ATGGTTTACGTCAGGTTTCAAGTTGTCTGTCAGACCTCTAGCTGTGATGAAGAAATC 487
DB 514 ATGGATATTGGCCAGCGCTCAGGTCGCTTGAAGTACACTCGCTGTATGAAGATC 573
QY 488 TTCAAGTTTCTCGCGTCAATGGCTGTCATGTTGTTTCTGAGTATCTTTTCTGA 547
DB 574 ATCAAGTTCTTCCAGTTATTGGCTGTCATGTTGTTGTCAGAGTACTCTNNNGGA 633
QY 548 GAGAAGTTGGCCCAAGGATGAAGACATTAAGTCAAGGATCCAGGATCCAGGATCTAGTAT 607
DB 634 AAGAGCTGGCCCAAGGATGAAGACATTAAGTGGGTCCTCAAGGTTGAAGACTT 693
QY 608 CCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAGGAACGCGTTTACACAGGCCAACT 667
DB 694 CCCTAGACCAATTTGGCTAGCTCTCTTTCTGTCAGGCTACTCGCTTTTACTCCAGCAAGCT 753
QY 668 ATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCTGTTCTCAGAAATGTTTGTAT 727
DB 754 TCTCGCAGCTCAGGAATATGCGGCTTCCAGGCTTACCGGCTCTCAGAAATGACTTAT 813
QY 728 TCCAAGAACTAAGGTTTCTGTCAGTAAGTATATGCGCTCATTTGTTCTGCGCAT 787
DB 814 TCCACGTACCAAGGATTTGATCTGTGTAAAGTATTATGCGAGATTTTGTTCAGCCAT 873
QY 788 TTATGATGAACAGTACGCAATCCCTAAGGTTCCCTGCTCTACATGCTAAGACTCTT 847
DB 874 TTATGATGAACCTGTATAGTCTTCAAGATTTCCCTCAACCAACTGCTCGGATTTT 933
QY 848 CAAGGACCAACCTTCAAGTGTGATGTTTATATCAAGAGGCAATTTGATGAAGGAATGCC 907
DB 934 GAAAGGCAATCATCATGATGATATGTCGCGATGAAGAGCTCATGCAATGAGTGAATGCC 993
QY 908 AGATACAGATGAGGCTTGTCTCAATGGTGTGAGATATATTGTGCGCAAGATGCTTT 967
DB 994 AAAATCAGATGAGGATGTTTCAAAATGGTGTAAAGACANNANNGTGGCAAGGATGCTTT 1053
QY 968 GTTAGACAAACATATGCTGAGGCTACTTTTACTGATCAAGAGCTCAGGATCTGGTCG 1027
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DB 1054 ACTGACAAGCATTTGGCAACAGGCACCTTT---CGATGAGGAGATTAGACCTATTGGCGG 1110
QY 1028 ACCAATAAAGTCTCTTCTGGTAGTTATATCTTGGCGCTGTCTGGTTGTTCGGGGTCTGT 1087
DB 1111 TCCAGTGAACATCTGCTGGTGACCCCTGTTCTGGTGGCTCTCTGCTGTTGGCGCAT 1170
QY 1088 AAGTTCTCTGCAATGCTTCTGTTACTCTCTCTGGAAGGCTGTGCAATTTACGCTTT 1147
DB 1171 CGAGTTCTTCAAGTGGACACAGCTTCTGACGCTGGAGGGGTGTGNNNNNNNNNNNN 1230
QY 1148 TGGTTTGGCAGTTGTTACTGCACATTATGCAAAATCTGATTCAATTCACAGTCAGAGG 1207
DB 1231 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1290
QY 1208 TTCAAAACCCGCCAAG 1223
DB 1291 GTGAGCTCAGCAGG 1306

BG585566 780 bp mRNA linear EST 11-APR-2001
EST487330 MHAM Medicago truncatula/Glomis versiforme mixed EST
library cDNA clone pMHAM-3018 5' end, mRNA sequence.
BG585566
BG585566.1 GI:13600630
EST:
Medicago truncatula/Glomis versiforme mixed EST library
Medicago truncatula/Glomis versiforme mixed EST library
Eukaryota; mixed EST libraries.
REFERENCE
1 (bases 1 to 780)
AUTHORS
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
and Fraser,C.M.
ESTs from roots of Medicago truncatula after colonization with
Glomis versiforme, 2001
JOURNAL
Unpublished (2001)
COMMENT
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N381040e TIGR sequence name: MTDGF52PK More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA GAA CTA gta gat CC).

FEATURES
source
Location/Qualifiers
1..780
/organism="Medicago truncatula/Glomis versiforme mixed EST
library"
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/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-3018"
/tissue_type="roots colonized with Glomis versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomis versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_hosts="E. coli strain XL0LR"
/clone_lib="MHAM"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomis versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-aseist
helper phage and propagated in XL0LR cells."
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Query Match

32.9%; Score 492.6; DB 12; Length 780;

/clone="SOYBEAN CLONE ID: Gm-c1057-4422"
/tissue type="Degenerating cotyledons, 2 week old
seedling"
/lab host="DH10B"
/clone_lib="Gm-c1057"

/note="vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 2 week old seedlings from
P1468916. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion.
The cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 31.2%; Score 468; DB 12; Length 564;
Best Local Similarity 89.4%; Pred. No. 1.4e-70;
Matches 504; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 450 GGTGTCCTGGCAGCAGCTAGCTGATGATCAAGAAATCTCAAGTTCTGCGGTCATT 509
DB 1 GGTGTCCTGGCAGCAGCTAGCTGATGATCAAGAAATCTCAAGTTCTGCGGTCATT 60
QY 510 GGCTGTCATATGTTTCTGAGTATCTTTTCTGGAGAGAAAGTTGGCCAGGATGAA 569
DB 61 GGTTGGTCAATGTGTTTCTGAATATCTTTCTCGAGAGAAAGTTGGCCAGGATGAA 120
QY 570 AGCATTAAAGTCAGCATCCAGCGATGATTCCTTCCTTCCTTCCTTCCTTCCTTC 629
DB 121 CGCATTAAAGTCAGCATCCAGCGATGATTCCTTCCTTCCTTCCTTCCTTCCTTC 180
QY 630 CTCTTTTGAAGAAAGCGCTTTTACACAGGCCAACTATTAGCTCTCAGAAATATGCC 689
DB 181 CTCTTTTGAAGAAAGCGCTTTTACACAGGCCAACTATTAGCTCTCAGAAATATGCA 240
QY 690 ACTTCCACTGATGCTGTTCTGAGAAATGTTTGAATTCAGAACTAAGGTTTGT 749
DB 241 GCCTCAGCTGATGCTGTTCTGAGAAATGTTTGAATTCAGAACTAAGGTTTGT 300
QY 750 TCTGCACTAGTATGCTGCTCATTTGTTCTGCGCAATTTATGATTAACAGTAGCATC 809
DB 301 TCAGCAGTAACCATATGCGCTGTTGTTCTGCGCAATTTATGATTAACAGTAGCATC 360
QY 810 CTTAAGATTCCTGCTGCTCAATGCTAAGACTCTTCAAGGACAACTTCAGTGTG 869
DB 361 CCCAAGAGTTTCACTGCTCTCAATGCTAAGACTCTTCAAGGACAACTTCAGTGTG 420
QY 870 CATGTTTCATATCAAGAGGATTTGATGAGGAACTGCCAGATACAGAGCTGTGCT 929
DB 421 CATGTCATATTAAGCGGATGCGATGAGGATTTGCCAGAAAGATGAACTGTGCT 480
QY 930 CAATGTTGTCGAGATATTTGTCGCAAGGATGCTTTTGTAGACAAACATATGCTGAG 989
DB 481 CAATGTTGTCGAGATGTTTGTGCGCAAGGATGCTTTTGTAGACAAACATATGCTGAG 540
QY 990 GGTACTTTTATGATCAAGAGCTG 1013
DB 541 GACACATTTAGTATCAAGAGCTG 564
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RESULT 10

AW508939

LOCUS

DEFINITION

Gm-r1030-1174 y1 Gm-r1030 glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-r1030-1174 5' similar to TR:Q40119 Q40119

1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE ;, mRNA sequence.

AW508939

VERSION

AW508939.1 GI:7147017

KEYWORDS

SOURCE
ORGANISM

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS

1 (bases 1 to 620)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvett, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, J., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE
JOURNAL

Contact: Shoemaker R/Public Soybean EST Project

COMMENT

Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35891 for further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 325.
Location/Qualifiers

FEATURES

source

1..620
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clones="GENOME SYSTEMS CLONE ID: Gm-r1030-1174"
/lab_host="DH10B"
/clone_lib="Gm-r1030"
/note="vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
cDNA library was constructed from mRNA isolated from
immature cotyledons of greenhouse grown plants
(individual seed fresh weight of 100-300mg). The library
was prepared using the Life Technologies pSuperScript cDNA
library construction kit. Complementary DNA was
synthesized from mRNA using a poly(dT) sequence with a
NotI restriction site. SalI linkers adapters were ligated
to the blunt-ended cDNA fragments followed by NotI
digestion. The cDNA fragments were directionally cloned
into the NotI-SalI restriction site of the pSPORT1
vector. The ligated cDNA fragments were transformed into
E. coli ElectroMax DH10B host cells. This library was
constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note
that Gm-r1030 is a re-rack of Gm-c1007."

ORIGIN

Query Match 31.1%; Score 465.4; DB 10; Length 620;
Best Local Similarity 86.2%; Pred. No. 3.9e-70;
Matches 514; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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QY 139 CAGCGGCGGTGGTACCATTTGGGCTGCTCTTCTTCGCTCCGGCTCTTGTAAATC 198
DB 25 CTGCAGTTGGTGGTCCCATTTGGGCTTCTTCTTCGCTCCGGCTCATCGTTAAC 84
QY 199 TCATTAGGCAATATGCTATGCTGTAAGCGGTGCGAAATTTGTACAGAGGA 258
DB 85 TCATTAGGCAATATGCTATGCTGCGGCGGTGCGAAATTTGTACAGAGGA 144
QY 259 TCACCGGCTAGTAGCAGAGCTCTTGTGGCTGAGCTGTATGCTTATTGTTGGG 318
DB 145 TGAACAGGTTGGTGGGAGCTCTCTGCTGAGAGCTGTGTGGATTATTGTTGGG 204
QY 319 CAGGAGTTAAGTCCAAATATTCACAGATCATGAACCTTTTGTATTAAGGTAAGAGC 378
DB 205 CCGGTGTTAAGTTCAGATTTTACAGATCCTGAAACCTTTTGTATTAAGGTAAGAGC 264
QY 379 ATGCACCTTGTGTAAGCAATTCACAGAGTCATATTCATTGGCTTGTGATGGTTTCA 438
```


Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 656 Std Error: 0.00
Plate: 100 Row: 6 Column: 06
Seq primer: TCACACGAAACAGCTATGAC.
Location/Qualifiers

FEATURES

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/clone_lib="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"

ORIGIN

Query Match 30.8%; Score 461.2; DB 10; Length 656;
Best Local Similarity 84.3%; Pred. No. 2e-69;
Matches 531; Conservative 0; Mismatches 98; Indels 1; Gaps 1;

QY 124 GCATGGCTATTGCAGACGGCCGTGGTGTACCATTTGGCCCTGCTCTCTTCGCTCGG 183
DB |||||
QY 184 GCGTCTTGTAACTCATTCAGCAATATGCTATGTCGCGAAGCCGGTTCGAAA 243
DB |||||
QY 70 GTCTCATCGTTAACTCATTCAGCAATATGCTATGTCGCGAAGCCGGTTCGAAA 129
DB |||||
QY 244 GTTTGTACAGAGATCAACCGGTGTAGTACAGAGCTCTTGTGCTGGAGCTGTATGCG 303
DB |||||
QY 130 ATTGTACAGAGATCAACCGGTGTAGTACAGAGCTCTTGTGCTGGAGCTGTATGCG 189
DB |||||
QY 304 TTATTGATGGTGGGAGGAGTTAAGTTCGCAATATTCAGATCATGATGAACCTTCGTT 363
DB |||||
QY 190 TTTTGTGATGGTGGGAGGAGTTAAGTTCGCAATATTCAGATCATGATGAACCTTCGTT 249
DB |||||
QY 364 TAATGGTAAAGAGATGCTGTTGATAGCAATACAGAGCTCTTGTGCTGGAGCTGTATGCG 423
DB |||||
QY 250 TCATGGGTACGAGCATGCTCTTGTGATATCCAAATACAGAGTGCATGATGCTGCTG 309
DB |||||
QY 424 TTGGATGGTTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 483
DB |||||
QY 310 TTGATGGAATTTAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 369
DB |||||
QY 484 AATCTTCAAGATTTCTGCGGTCATTTGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 543
DB |||||
QY 370 AATCATCTAAGTTTCTGCGGTCATTTGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 429
DB |||||
QY 544 TGGAGAGAGTTGGGCAAGATGAAAGACATTTAAAGTCAGGATCCAGGCACTGAGTG 603
DB |||||
QY 430 TGGAGAGAGTTGGGCAAGATGAAAGACATTTAAAGTCAGGATCCAGGCACTGAGTG 489
DB |||||
QY 604 ATTTCCCTCTTCCTTTTGGCTAGCTCTCTTTTGAAGAAAGCGGTTTACAGAGCA 663
DB |||||
QY 490 ATTTCCCTCTTCCTTTTGGCTAGCTCTCTTTTGAAGAAAGCGGTTTACAGAGCA 549
DB |||||
QY 664 AACTATTAGCTGCTCAGGATATGCCACTTCCACTGATTTGCTGTTCTAGAAATGTTT 723
DB |||||
QY 550 AATTATTAGCGCTCAGGATATGCCACTTCCACTGATTTGCTGTTCTAGAAATGTTT 723
DB |||||
QY 724 TGA-TTCCAGAACTAAGGGTTTGTGTTCT 752
DB |||||
QY 610 TGATTTCCAGAACTAAGGGGGTTTGTGTTCT 639
DB |||||

RESULT 13
CD400176/c

LOCUS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

CD400176 466 bp mRNA linear EST 07-JUN-2003
GM_CK21948 Soybean induced by Salicylic Acid Glycine max cDNA 3',
mRNA sequence.
CD400176
CD400176.1 GI:31458148
EST.
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 466)
Tian,A.-G., Wang,J., Cui,P., Han,Y.-J., Xu,H., Cong,L.-J.,
Huang,X.-G., Wang,X.-L., Jiao,Y.-Z., Wang,B.-J., Wang,Y.-J.,
Zhang,J.-S., Chen,S.-Y. and Yu,J.
Soybean Expressed Sequence Tags Sequencing
Unpublished (2003)
Contact: Chen S-Y
Plant Biotechnology Laboratory
Institute of Genetics and Developmental Biology, CAS, China
Datun road, Beijing 100101, China
Tel: 86-10-64886859
Fax: 86-10-64873428
Email: sychen@genetics.ac.cn
Email: sychen@genetics.ac.cn
Seq primer: T7 primer.
Location/Qualifiers
1..466
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/mol_type="mRNA"
/cultivar="Kefeng 1"
/db_xref="taxon:3847"
/tissue_type="Seedlings"
/dev_stage="two-week seedlings"
/lab_host="XLI-Blue MRF strain"
/clone_lib="Soybean induced by Salicylic Acid"
/note="Vector: pBluescript SK+; Site 1: EcoR I; Site 2:
Xho I; The cDNA library was constructed by He, C-Y from
mRNA isolated from two-week seedlings (cultivar Kefeng 1)
treated by spraying 2.0mM salicylic acid for 24, 36, 48
and 72 h. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into XLI-Blue MRF
host cells (Stratagene)."

ORIGIN

Query Match 29.6%; Score 442.8; DB 14; Length 466;
Best Local Similarity 99.3%; Pred. No. 3.3e-66;
Matches 455; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1020 ACTGGTCGACCAATAAGTCTCTCTGCTAGTATATCTTGGCGTCTCTGGTGTGCG 1079
DB |||||
QY 458 ACTGGTCGACCAATAAGTCTCTCTGCTAGTATATCTTGGCGTCTCTGGTGTGCG 399
DB |||||
QY 1080 GGGTCTGTAAGTTCCTCGCAATGCTCTTCTTACTCTCTTCTCGGAGGGTGTGCAATT 1139
DB |||||
QY 398 GGGTCTGTAAGTTCCTCGCAATGCTCTTCTTACTCTCTTCTCGGAGGGTGTGCAATT 339
DB |||||
QY 1140 TCAGCTTTGGTGGCAGTTGTACTGCACTTATGCAAAATCTGATTCGAATCTCACAG 1199
DB |||||
QY 338 TCAGCTTTGGTGGCAGTTGTACTGCACTTATGCAAAATCTGATTCGAATCTCACAG 279
DB |||||
QY 1200 TCAGAGGCTTCAAAACCGCGCAAGATCGTCTGCAAGTCAAAACCAAGGGGCTTGA 1259
DB |||||
QY 278 TCAGAGGCTTCAAAACCGCGCAAGATCGTCTGCAAGTCAAAACCAAGGGGCTTGA 219
DB |||||
QY 1260 TTTATTTGGCGAACTTAAAGTTGCAATTATGCTGATGAGTGAATGATTAATCACTCAT 1319
DB |||||

218 TTTATTGGCGAACTTAAAGTTGCATTTATGTGTGATGAGTCACTCATGTAATCACTCA 159
QY 1320 ATTTTGGCTTCAACATCTTATCAATAGTATGCTTCTATCTATATATATATATATGAAT 1379
Db 158 ATTTTGGCTTCAACATCTTATCAATAGTATGCTTCTATCTATATATATATATGAAT 99
QY 1380 GCTTATCGATTCATGTTTAAATTAATTAGGATATCCCTTTGTTGATTTAGACGTCTAGGG 1439
Db 98 GCTTATCGATTCATGTTTAAATTAATTAGGATATCCCTTTGTTGATTTAGACGTCTAGGG 39
QY 1440 GATGGC-CTGAGAAAATCAACCACTTATTTATTTTA 1476
Db 38 GATGGCACTAGAAAATCAACCACTTATTTATTTTA 1

RESULT 14
CB970126 670 bp mRNA linear EST 30-APR-2003
LOCUS CAB10003_Ila_Fa_D05 Cabernet Sauvignon Flower Pre-bloom - CAB1
DEFINITION Vitis vinifera cDNA clone CAB10003_Ila_Fa_D05 5', mRNA sequence.
ACCESSION CB970126
VERSION CB970126.1 GI:30252575
KEYWORDS EST
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 670)
Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and
Cook, D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon',
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6361
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGTACCGACATATGCC.
Location/Qualifiers
1..670
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB10003_Ila_Fa_D05"
/sex="Hermaphrodite"
/dev_stage="Pre-bloom"
/lab_host="DH5alpha"
/clone_lib="Cabernet Sauvignon Flower Pre-bloom - CAB1"
/notes="Organ: Flower - Pre-bloom; Vector: pDNR; Site 1:
Sfil; Site 2: Sfil; CAB1 is a cDNA library of Vitis
vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples
were collected approximately eleven days before onset of
bloom (clusters at this stage were fully developed and
flowers with calyptras or caps still attached. Sampled
vines were located at the University of California, Davis,
Experimental Vineyard. cDNAs were made by oligo-dT priming
and directionally cloned. 5' and 3' adaptors were used in
cloning as follows:
5'-AAGCATGTGATACAGCGAGTGGCCATACGGCCGG-3' and
5'-ATTCTAGCGCCGAGCGCGCATG-dt(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

Query Match 29.1%; Score 436.4; DB 14; Length 670;
Best Local Similarity 81.2%; Pred. No. 3.5e-85;
Matches 506; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
ORIGIN

QY 122 GGGCATGGCTATTGCGAGAGCGCGGTGGTGTACATTTGGGCCCTGCTCTCTTTCGCCCTC 181
Db 48 GGATATGGCGATTGCGAGCGGCTGCGGTTGCCGTTCCGCTGGGCTTCTCTTCTCCACCTC 107
QY 182 CGGCTCTCTTGTATATCTCATTCAGGCAATATGCTATGTCGTCGTAAGSCGCGTGTGAA 241
Db 108 CGGCTCTGTAGTATATCTCATTCAGGCAATATGCTATGTCGTCGTAAGSCGCGTGTGAA 167
QY 242 AAGTTTGTACAGAGGATCAACCGGTTAGTACAGAGCTTCTTGGCTGGAGCTTGTATG 301
Db 168 AAGTACATACAGAGGATCAACAGAGTGTAGCAGAAATTTATTTGGCTCGAGCTTGTGTG 227
QY 302 GCTTATTTGATTTGGTGGCAGGATTAAGTCCAAATATTCACAGATCATGAACCTTTTCG 361
Db 228 GCTTATTTGATTTGGTGGCAGGATTAAGTCCAAATATTCACAGATCATGAACCTTTTCG 287
QY 362 TTTAATGGTAAAGAGCATGCACTTTGTGATAAGCAATCACAGAACTGATATTGTTGGCT 421
Db 288 CTTAATGGTAAAGAAACATGCACTTCTTTATATCAAAACACAGAACTGACATTTGTTGGCT 347
QY 422 TCTTGGATGGGTTTCAGCTCAGCTTCCAGTTTCTTTGGCAGCACTTAGCTGTGATGAA 481
Db 348 TCTTGGATGGGTTTGGCTCAGCATCAGGTTGCTTGGCAGCACTTAGCTGTGATGAA 407
QY 482 GAAATCTTCAAAGTTTCTGCCGCTCATTTGGCTGGTCAATGTGGTCTTCTGAGTATCTTTT 541
Db 408 GAAATCATCAAAATTCCTTCCGGTATAGTTGGTCAATGTGGTCTTCTGAGTATTTATT 467
QY 542 TCTGAGAGAGTCTGGGCCAAGATGAAGACATTAAGTCAGGATCCAGCGACTGAG 601
Db 468 TCTGAGAGAGAACTGGGCCAAGATGAAGACATTAAGTCAGGATCCAGCGACTGAG 527
QY 602 TGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAGGAAACGCGTTTACACAGGC 661
Db 528 GGACTACCTCAGCCTTTTGGTGGCTCTTTTGGTGGGAACTCCCTTTACACAGGC 587
QY 662 CAACTATTAGTCTGCTCAGGAATATGCCATTCACATGCTGATTTGCTGTCTAGAAATGT 721
Db 588 NAAAGCTTTTAGCAGCTCAAGAATATGCAACTGCATCGGGTTCCTGTCTTAGAAATGT 647
QY 722 TTTGATTTCCAGAACTAAGGTTT 744
Db 648 TCTGATTTCCCGTACTAAGGTTT 670

RESULT 15
BQ403131 585 bp mRNA linear EST 22-MAY-2002
LOCUS GA_Ed0054C03f Gossypium arboreum 7-10 dpa fiber library Gossypium
DEFINITION arboreum cDNA clone GA_Ed0054C03f, mRNA sequence.
ACCESSION BQ403131
VERSION BQ403131.1 GI:21090818
KEYWORDS EST
SOURCE Gossypium arboreum
ORGANISM Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 685)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,
Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 521
Seq primer: TAATACGACTCACTATAGG

High quality sequence start: 3
High quality sequence stop: 637.
FEATURES
 source
 1. .685
 /organism="Gossypium arboreum"
 /mol_type="mRNA"
 /strain="AXA"
 /cultivar="8400"
 /db_xref="taxon:29729"
 /clone="GA_Ed0054C03f"
 /tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
 /lab_host="E. coli"
 /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
 /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 29.0%; Score 434.4; DB 13; Length 685;
Best Local Similarity 79.2%; Pred.No. 7.7e-65;
Matches 513; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Qy 111 TGGGCTGGGCTGGGCTGCTATTGACAGACGCGCGTGGTGTACCATTTGGGCGCTGCTC 170
Db |||||
Qy 38 TTGGCTGTTCTGCTCCATGGCGATGACGCGGAGCTGTTATCTCCATTTGGGCGCTTCTT 97
Db |||||
Qy 171 TTCCTCGCCTCCGCGCTCCTTTGTTAATCTCATTGAGCAATATGCTATGTCGCTGAAGG 230
Db |||||
Qy 98 TTCTTCATCTCCGCGCTCGCTGTGATCTCATTGAGGAGTATGCTTTGTTCTTATTGGA 157
Db |||||
Qy 231 CCGGTGTCGAAAGTTGTACAGAGGATCAACCGGTAGTAGCAGAGCTCTTGTGGCTG 290
Db |||||
Qy 158 CCACGTGCCAAGAACACATATAGAAAGATCAATAGGGTATTTGGCAGAGTTGTTGTGGCTG 217
Db |||||
Qy 291 GAGCTTGTATGGCTTATTGATTGTTGGGCGAGGATTAAGGTCCTCAATATTTACAGATCAT 350
Db |||||
Qy 218 CAAGTGGTTTGGCTGGTTGATTGGTGGCGAGCGGTTAAGATTGAAGTTTCGAGATCAT 277
Db |||||
Qy 351 GAACCTTTTCGTTTAAATGGGTAAGAGCATGCACTTGTGATAAGCAATCACAGAATGAT 410
Db |||||
Qy 278 GAAAGCTTCAATTTAATGGGTAGGAACATGCCCTTTGTCATATGCAATCACAGAATGAT 337
Db |||||
Qy 411 ATTGATTGGCTTGTGGATGGTTTCAGCTCAGGTTTCAGGTTGTCTTGGCAGCACTCTA 470
Db |||||
Qy 338 ATTGATTGGTTAGTTGGATGGGTTTACACAGAGGTCAGGTTGTCTTGGCAGTACATTA 397
Db |||||
Qy 471 GCTGTGATGAGAAATCTTCAAGTTTCTCCGGTCAATTCGGCTGGTCAATGTGTTTCT 530
Db |||||
Qy 398 GCTGTATGAAGAAATCATCAAAATTCCTCCGGTCATAGGTTGGTCAATGTGTTTCT 457
Db |||||
Qy 531 GAGTATCTTTTCTGGAGAGAGTTGGCCAGAGATGAAGACATTAAGTCAGGCATC 590
Db |||||
Qy 458 GAGTATCTGTTTGGAAACGAGCTGGCCAGAGATGAAGAACACATTAAGGCGAGTCTT 517
Db |||||
Qy 591 CAGGAGCTGAGTATTCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGAAACCGGT 650
Db |||||
Qy 518 CAACGTTTAAAGGACTTCCACAGGCCATTTTGGTTGGCACTTTTGTAGAAGGAACCTNG 577
Db |||||
Qy 651 TTTACAGGCGCAACTATTAGTGTCTCAGGAATATGCCACTTCCACTGGATTGCTGTT 710
Db |||||
Qy 578 TTTACAGCAAGCAAGCTTCTAGCAGCTCAAGATATGCAACCTCACAGGATTGCTGTGA 637
Db |||||
Qy 711 CCTAGAAATGTTTCATTCCAAAGAACTAAGGGTTTCTTCTGCACTA 758
Db |||||
Qy 638 CCTAATAATGTTTAAATTCCTCGTACAAAGGGTTTCTTTCANCCGTA 685
Db |||||

OM protein - protein search, using sw model
Run on: July 7, 2004, 13:36:58 ; Search time 45 seconds
(without alignments)
2643.341 Million cell updates/sec

Title: US-09-914-098-56
Perfect score: 1935
Sequence: 1 MAIAAAVVVPJGLLFFASG.....QSERNPAAKIVPAKSKNKGS 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archesp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1567	81.0	390	10 Q9XFW4	Q9xw4 brassica na
2	1564	80.8	389	10 Q8LG50	Q8lg50 arabidopsis
3	1519	78.5	377	10 Q40119	Q40119 linanthus
4	1450.5	75.0	374	10 Q41745	Q41745 zea mays (m
5	1336	69.0	306	10 Q9SDN3	Q9sdn3 prunus dulc
6	1277	66.0	376	10 Q9SYC8	Q9syc8 arabidopsis
7	1161.5	60.0	310	10 Q9SVX9	Q9svx9 arabidopsis
8	1156.5	59.8	311	10 Q93317	Q93317 brassica na
9	844.5	43.6	237	10 Q7X9L2	Q7x9l2 triticum ae
10	606	31.3	376	11 Q9D517	Q9d517 m adult mal
11	599	31.0	376	11 Q7TT39	Q7tt39 mus musculu
12	595.5	30.8	376	13 Q7ZY11	Q7zy11 xenopus lae
13	595	30.7	386	5 Q9VV51	Q9vv51 drosophila
14	587	30.3	377	13 Q7ZWC9	Q7zwc9 brachydanio
15	579	29.9	380	5 Q9VV49	Q9vv49 drosophila
16	551.5	28.5	378	11 Q8K4X7	Q8k4x7 m lysophosp

17	502.5	26.0	314	11 Q8BST2	Q8bst2 mus musculu
18	441	22.8	399	10 Q8LQ83	Q8lq83 oryza sativ
19	415	21.4	378	10 Q8LY2	Q8ly2 arabidopsis
20	414	21.4	373	10 Q9SSH0	Q9ssh0 arabidopsis
21	414	21.4	393	10 Q9C9P8	Q9c9p8 arabidopsis
22	400	20.7	375	10 Q9LHN4	Q9lhn4 arabidopsis
23	310.5	16.0	350	3 Q94361	Q94361 schizosacch
24	287	14.8	344	5 Q16526	Q16526 caenorhabdi
25	269	13.9	386	5 Q9SR12	Q9sr12 caenorhabdi
26	253.5	13.1	399	5 Q23087	Q23087 caenorhabdi
27	250	12.9	439	5 Q20800	Q20800 caenorhabdi
28	235.5	12.2	308	4 Q8N1Q7	Q8n1q7 homo sapien
29	202.5	10.5	281	5 Q8SS20	Q8ss20 encephalito
30	187	9.7	357	5 Q8SR20	Q8sr20 encephalito
31	180.5	9.3	370	11 Q91YX5	Q91yx5 mus musculu
32	176.5	9.1	404	13 Q7ZT38	Q7zt38 xenopus lae
33	173	8.9	300	16 Q83A38	Q83a38 coxiella bu
34	172	8.9	295	16 Q88R02	Q88r02 pseudomonas
35	168.5	8.7	299	16 Q88AE0	Q88ae0 pseudomonas
36	162	8.4	292	16 Q87KC2	Q87kc2 vibrio para
37	160.5	8.3	304	16 Q91SA6	Q91sa6 pseudomonas
38	148	7.6	310	16 Q8X8H2	Q8x8h2 escherichia
39	148	7.6	318	16 Q8FSH4	Q8fsh4 escherichia
40	145.5	7.5	296	16 Q83FB3	Q83fb3 coxiella bu
41	144	7.4	310	16 Q7UB62	Q7ub62 shigella fl
42	144	7.4	318	16 Q83IV6	Q83iv6 shigella fl
43	143	7.4	415	5 Q01882	Q01882 caenorhabdi
44	142.5	7.4	300	16 Q8XOC1	Q8xoc1 ralstonia s
45	135.5	7.0	428	5 Q95R03	Q95r03 caenorhabdi

ALIGNMENTS

RESULT 1
Q9XFW4
ID Q9XFW4 PRELIMINARY; PRT; 390 AA.
AC Q9XFW4;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE Acyl-CoA:1-acylglycerol-3-phosphate acyltransferase
DE (EC 2.3.1.51).
GN LPAAT.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Developing siliques;
RA Graefin zu Muenster A., Wolter F.P., Frentzen M.;
RT "A cDNA encoding a microsomal 1-acylglycerol-3-phosphate
RT acyltransferase of Brassica napus L.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z95637; CAB09138.1;
DR GO; GO:0003841; F:1-acylglycerol-3-phosphate O-acyltransferase. . . ; IEA.
DR GO; GO:0008445; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002123; Acyltransferase.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; F1SC; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Acyltransferase; Transferase.
SQ SEQUENCE 390 AA; 43771 MW; F1446E1B30009C37 CRC64;

Query Match 81.0%; Score 1567; DB 10; Length 390;

Best Local Similarity 77.8%; Pred. No. 2.9e-131;

Matches 288; Conservative 43; Mismatches 39; Indels 0; Gaps 0;

QY 5 AAATVPLGLFFASGLLVNLIQAI CYVVVRPVSKSLYRINRVVAELLWLELVWIDW 64
 DB 4 AAATVPLGLFFISGLLVNLIQAVCYLVPRPNKNTYRKINRVVAETLWLELVWIDW 63
 QY 65 AGVKVQIETDHEFTFLMGKEHALVINSRSDIDWLVGVWSAORSGLGSLTAVMKKSKF 124
 DB 64 AGVKIQUFADDEFNMGKEHALVVCNHRSDIDWLVGVWLAORSGLGSLTAVMKKSKF 123
 QY 125 LPVIGSMWFSEYLFPLERSWAKDESTLKGISQRLSDPFLPFWLALFVEGTRFTQAKLAA 184
 DB 124 LPVIGSMWFSEYLFPLERNWAKDESTLQSGQLRLNDFPFPFWLALFVEGTRFTQAKLAA 183
 QY 185 QEYATSGLPVPRNVLIPTKGFVSASVSMRSPVPAIYDVTVAPKSSPAPTMLRLFKQ 244
 DB 184 QEYAAASSELPIPRNVLIPTKGFVSASVSMRSPVPAIYDVTVAPKSSPAPTMLRLFKQ 243
 QY 245 PSVVHVIKHELMKELPDTDEAVACQCRDIFVAKDALLDKHNAEGTFSQEQ-LDTGRPIK 304
 DB 244 PSVVHVIKHELMKELPDTDEAVACQCRDIFVAKDALLDKHNAEGTFSQEQ-LDTGRPIK 303
 QY 305 SILVWISWACLVVAGSVKFLQSSLLSSWKGAFSAFGLAVVTALMQILIQFSQSERSNP 364
 DB 304 SILVWISWACLVVAGSVKFLQSSLLSSWKGAFSAFGLAVVTALMQILIQFSQSERSNP 363
 QY 365 AKIVPAKSKN 374
 DB 364 AKVAPAKPKD 373

RESULT 2
 Q8LG50 PRELIMINARY; PRT; 389 AA.
 AC Q8LG50
 DT 01-OCT-2002 (T-REMBLrel. 22, Created)
 DT 01-OCT-2002 (T-REMBLrel. 22, Last sequence update)
 DE 1-acyl-sn-glycerol-3-phosphate acyltransferase-like protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volkovsky N., Town C.D., Troughan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY844461; AAM61033.1;
 DR GO; GO:0008415; F:acyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002123; Acyltransferase.
 DR Pfam; PF01553; Acyltransferase; 1.
 DR SMART; SM00563; PlcC; 1.
 DR PROSITE; PS00038; HLH_1; 1.
 DR Acyltransferase; Transferase.
 KW Acyltransferase; Transferase.
 SQ SEQUENCE 389 AA; 43706 MW; F34F73B2E2AC6837 CRC64;
 Query Match 80.8%; Score 1564; DB 10; Length 389;
 Best Local Similarity 76.9%; Pred. No. 5.4e-131;
 Matches 286; Conservative 43; Mismatches 43; Indels 0; Gaps 0;
 QY 3 AAATVPLGLFFASGLLVNLIQAI CYVVVRPVSKSLYRINRVVAELLWLELVWIDW 62

DB 2 VIAAAVIVPLGLFFISGLLVNLIQAVCYLVIRPLSKNTYRKINRVVAETLWLELVWIDW 61
 QY 63 WAGVKVQIETDHEFTFLMGKEHALVINSRSDIDWLVGVWSAORSGLGSLTAVMKKSS 122
 DB 62 WAGVKIQUFADDEFNMGKEHALVVCNHRSDIDWLVGVWLAORSGLGSLTAVMKKSS 121
 QY 123 KFLPVIKSMWFSEYLFPLERSWAKDESTLKGISQRLSDPFLPFWLALFVEGTRFTQAKLL 182
 DB 122 KFLPVIKSMWFSEYLFPLERNWAKDESTLKGISQRLSDPFLPFWLALFVEGTRFTQAKLL 181
 QY 183 AAQYATSGLPVPRNVLIPTKGFVSASVSMRSPVPAIYDVTVAPKSSPAPTMLRLFK 242
 DB 182 AAQYAAASSELPIPRNVLIPTKGFVSASVSMRSPVPAIYDVTVAPKSSPAPTMLRLFK 241
 QY 243 GQPSVHVIKHELMKELPDTDEAVACQCRDIFVAKDALLDKHNAEGTFSQEQ-LDTGRP 302
 DB 242 GQPSVHVIKHELMKELPDTDEAVACQCRDIFVAKDALLDKHNAEGTFSQEQ-LDTGRP 301
 QY 303 IKSLVWISWACLVVAGSVKFLQSSLLSSWKGAFSAFGLAVVTALMQILIQFSQSERS 362
 DB 302 IKSLVWISWACLVVAGSVKFLQSSLLSSWKGAFSAFGLAVVTALMQILIQFSQSERS 361
 QY 363 NPAAIVPAKSKN 374
 DB 362 TPAAKVPAPKPKD 373

RESULT 3
 Q40119 PRELIMINARY; PRT; 377 AA.
 AC Q40119
 DT 01-NOV-1996 (T-REMBLrel. 01, Created)
 DT 01-NOV-1996 (T-REMBLrel. 01, Last sequence update)
 DE 1-acyl-sn-glycerol-3-phosphate acyltransferase (Putative).
 OS Limnathes douglasii (Douglas's meadowfoam).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Limnathaceae; Limnathes.
 OX NCBI_TaxID=28973;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96045746; PubMed=7579178;
 RA Brown A.P., Brough C.I., Kroon J., Slabas A.R.;
 RT "Identification of a cDNA that encodes a 1-acyl-sn-glycerol-3-
 RT phosphate acyltransferase from Limnathes douglasii.";
 RL Plant Mol. Biol. 29:267-278(1995).
 DR EMBL; Z48730; CAA88620.1;
 DR PIR; S60478; S60478;
 DR GO; GO:0008415; F:acyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002123; Acyltransferase.
 DR Pfam; PF01553; Acyltransferase; 1.
 DR SMART; SM00563; PlcC; 1.
 DR PROSITE; PS00038; HLH_1; 1.
 DR Acyltransferase; Transferase.
 KW Acyltransferase; Transferase.
 SQ SEQUENCE 377 AA; 42780 MW; 0DECEDEF25D39687C CRC64;
 Query Match 78.5%; Score 1519; DB 10; Length 377;
 Best Local Similarity 77.0%; Pred. No. 5.3e-127;
 Matches 282; Conservative 43; Mismatches 41; Indels 0; Gaps 0;
 QY 1 MAIAAAVVPVPLGLFFASGLLVNLIQAI CYVVVRPVSKSLYRINRVVAELLWLELVW 60
 DB 1 MAIAAAVVPVPLGLFFASGLLVNLIQAI CYVVVRPVSKSLYRINRVVAELLWLELVW 60
 QY 61 IDWAGVKVQIETDHEFTFLMGKEHALVINSRSDIDWLVGVWSAORSGLGSLTAVMKK 120
 DB 61 IDWAGVKVQIETDHEFTFLMGKEHALVINSRSDIDWLVGVWSAORSGLGSLTAVMKK 120

Db 121 SSKFLPVIGSWMFSEYFLERNWAKDENTLKSGLQRLNDPKPFWLALFVEGTRFTAK 180
Qy 181 LLAQAEYATSTGLPVRNVLIIPRTKGFVSASHMSFVPAIYDVTVAIKSPAPMTLRL 240
Db 181 LLAQAEYASAGLPVRNVLIIPRTKGFVSASHMSFVPAIYDVTVAIKSPAPMTLRL 240
Qy 241 FKQPSVVHVIKRLHMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDBQLQDTG 300
Db 241 FKQSSVVHVLKRLHMKDLPTDDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVDIG 300
Qy 301 RPKSLVWISWACLWVAGSVFLOWSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360
Db 301 RPKSLVWISWACLWVAGSVFLOWSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360
Qy 361 RSNPAK 366
Db 361 HSTPAK 366

RESULT 4
Q41745
ID Q41745 PRELIMINARY; PRT; 374 AA.
AC Q41745;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 1-acyl-glycerol-3-phosphate acyltransferase (Putative).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_taxid=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Black Mexican Sweet; TISSUE=Endosperm;
RX MEDLINE=9503593; PubMed=7948871;
RA Brown A.P., Coleman J., Tomney A.M., Watson M.D., Slabas A.R.;
RT "Isolation and characterization of a maize cDNA that complements a 1-
RT acyl sn-glycerol-3-phosphate acyltransferase mutant of E.coli and
RT encodes a protein which has similarities to other acyltransferases.";
RL Plant Mol. Biol. 26:211-223 (1994).
RL EMBL; Z29518; CAA82638.1; -.
DR PIR; S52645;
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001213; Acyltransferase.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; P1SC; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Acyltransferase; Transferase.
SQ SEQUENCE 374 AA; 42571 MW; 1F5492CAFF24F93 CRC64;

Query Match 75.0%; Score 1450.5; DB 10; Length 374;
Best Local Similarity 70.7%; Pred. No. 6.8e-121;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

Qy 1 MAIAAAVVPGLLFFAGLLVNLQACVYVVRPVSKSLYRRINRVVAELLWLVL 60
Db 1 MAIPLVLVLPGLLFLSLVINAQVLFVTVIRPFKSFYRRINRFLAELLWLQV 60
Qy 61 IDWAGVKVQIPDTHETFLMGKEHALVINSRSDIDWLVGWVSAORSGLSTLAVMK 120
Db 61 VDWAGVKVQLHADETYSMGKEHALVINSRSDIDWLVGWVSAORSGLSTLAVMK 120
Qy 121 SSKFLPVIGSWMFSEYFLERNWAKDENTLKSGLQRLNDPKPFWLALFVEGTRFTAK 180
Db 121 SSKFLPVIGSWMFSEYFLERNWAKDENTLKSGLQRLNDPKPFWLALFVEGTRFTAK 180
Qy 181 LLAQAEYATSTGLPVRNVLIIPRTKGFVSASHMSFVPAIYDVTVAIKSPAPMTLRL 240

Db 181 LLAQAEYASAGLPVRNVLIIPRTKGFVSASHMSFVPAIYDVTVAIKSPAPMTLRL 240
Qy 241 FKQPSVVHVIKRLHMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDBQLQDTG 300
Db 241 LKQSSVVHVRKRMHSEMPKSDSDVSKWCKDIFVAKDALLDKHLATGTF-DEETRPIC 239
Qy 301 RPKSLVWISWACLWVAGSVFLOWSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360
Db 300 RPKSLVWISWACLWVAGSVFLOWSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360
Qy 361 RSNPAKIPAKSKNK 375
Db 360 RSSARAARNVRKKE 374

RESULT 5
Q9SDN3
ID Q9SDN3 PRELIMINARY; PRT; 306 AA.
AC Q9SDN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 1-acyl-sn-glycerol-3-phosphate acyltransferase.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Eudicotyledons; core eudicots; Rosids;
OC eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_taxid=3755;
RN [1]
RP SEQUENCE FROM N.A.
RA Campalans A.; Pages M.; Messeguer R.;
RT "Identification of differentially expressed genes during dehydration
RT in almond (Prunus amygdalus) using the cDNA-AFLP technique.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213937; AAF20003.1; -.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001213; Acyltransferase.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; P1SC; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Acyltransferase; Transferase.
SQ SEQUENCE 306 AA; 33993 MW; CBD334496E25908D CRC64;

Query Match 69.0%; Score 1336; DB 10; Length 306;
Best Local Similarity 84.5%; Pred. No. 8.5e-111;
Matches 250; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

Qy 81 MGKEHALVINSRSDIDWLVGWVSAORSGLSTLAVMKSSKFLPVIGSWMFSEYFL 140
Db 1 MGKEHALVINSRSDIDWLVGWVSAORSGLSTLAVMKSSKFLPVIGSWMFSEYFL 60
Qy 141 ERSWAKDESTLKSGIQRSLDPPFLFWLALFVEGTRFTQAKLLAAQAEYATSTGLPVRNV 200
Db 61 ERSWAKDEGTLKSGVQRKLPQFPFWLALFVEGTRFTQAKLLAAQAEYATSTGLPVRNV 120
Qy 201 IPRTKGFVSASHMSFVPAIYDVTVAIKSPAPMTLRLFKGOPSVVHVIKHELMKEL 260
Db 121 IPRTKGFVTVSQMRSPAPAIYDVTVAIKSPAPMTLRLFKGOPSVVHVIKHELMKEL 180
Qy 261 PDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDBQLQDTGTRPIKSLVWISWACLWV 320
Db 181 PETDEAVAQWCKDIFVAKDALLDKHVEQTFGQDLKVTGRPLKSLVWVTAWACLLILGA 240
Qy 321 VKFQLQWSLLSSWKGVAFAFGLAVVTALMQILIQFSQSERNPAKIPAKSKNK 376
Db 241 LKFLYWSLLSSWKGVAFAFGLAVVTALMQILIRFQSQRSTPAPVAPTNKKNK 296

RESULT 6
Q9SYC6

DE Q9SYC8 PRELIMINARY; PRT; 376 AA.
AC Q9SYC8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative acyl-CoA:1-acylglycerol-3-phosphate acyltransferase.
GN F11M5.12
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A.; Palm C.J.; Conway A.B.; Conn L.; Hansen N.F.;
RA Altafi H.; Araujo R.; Huizar L.; Rowley D.; Buehler E.; Dunn P.;
RA Gonzalez A.; Kremenetskaia I.; Kim C.; Lenz C.; Li J.; Liu S.;
RA Luros S.; Schwartz J.; Shinn P.; Toriumi M.; Vysotskaia V.S.;
RA Walker M.; Xu G.; Ecker J.; Theologis A.; Davis R.W.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC060685; AAD30638.1; -
DR PIR; D96550.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002123; Acyltransferase.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; PlSC; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR Acyltransferase; Transferase.
KW Acyltransferase; Transferase.
SQ SEQUENCE 376 AA; 43435 MW; 0B9AE143B09ED4D0 CRC64;
Query Match 66.0%; Score 1277; DB 10; Length 376;
Best Local Similarity 62.3%; Pred. No. 2e-105;
Matches 228; Conservative 62; Mismatches 76; Indels 0; Gaps 0;
QY 1 MATAAAVVVPLGLLFFASGLLVNLIQAICYVVPVSKSLYRRINRVVAELLWLEVL 60
Db 1 MKIPAAVFPVGVFLISGLIWNILQLVFFIIVRPFSSLYRRINKNVALLQLIWL 60
QY 61 IDWAGVKVQIFDTHETFLRMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSTLAVNKK 120
Db 61 FDMWACKINLYVDAETLELIGKEHALVISNHRSDIDWLVGWSAQRSGCLGSTLAVNKK 120
QY 121 SSFLEPVGWSWMFSEYFLERSWAKDESTLKSGLQRLSDPPLFWLALFVEGTRFTQAK 180
Db 121 EAKYLPVGWSWMFSEYFLERSWAKDENTLKGFKLEDFPFWLALFVEGTRFTQAK 180
QY 181 LLAQYATSTGLPVRNVLIPRTKGFVSASHMSRFPVPAIYDVTVAI PKSSPAPTMRL 240
Db 181 LEAAQYATSTGLPVRNVLIPRTKGFVSASHMSRFPVPAIYDVTVAI PKSSPAPTMRL 240
QY 241 FKQPSVHVHVKHRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTSDQELQDTG 300
Db 241 FSCQSEINLQWRHKKSELPTDDGIAQWQDLITKDAQLEKFTKDVFSDLVHQIN 300
QY 301 RPIKSLVVISWACLAVAGSVKFLQWSLLSKWGVAFSAFLAVVATMALMOILIOFSQSE 360
Db 301 RPIKPLIVVIMGLFVFGFKLLQWLSIVASWKIILLFVFLVATITMTQILIOSSSQ 360
QY 361 RSNPAK 366
Db 361 RSTPAK 366

RESULT 7

Q9SVX9

ID Q9SVX9 PRELIMINARY; PRT; 310 AA.

AC Q9SVX9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE 1-acylcerol-3-phosphate acyltransferase-like protein.
GN F15B8.160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V.; Rechmann S.; Borkova D.; Ansoorge W.; Mewes H.W.;
RA Mayer K.F.X.; Lemcke K.; Schueller C.; Quetier F.; Salancubut M.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049660; CAB41190.1; -
DR PIR; T06755; T06755.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002123; Acyltransferase.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; PlSC; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR Acyltransferase; Transferase.
KW Acyltransferase; Transferase.
SQ SEQUENCE 310 AA; 34382 MW; A1B5748F37B625AD CRC64;
Query Match 60.0%; Score 1161.5; DB 10; Length 310;
Best Local Similarity 61.3%; Pred. No. 3.1e-95;
Matches 228; Conservative 30; Mismatches 35; Indels 79; Gaps 1;
QY 3 IAAAVVPLGLLFFASGLLVNLIQAICYVVPVSKSLYRRINRVVAELLWLEVL 62
Db 2 VIAAAVPLGLLFFISGLVNLV----- 25
QY 63 WAGVKVQIFDTHETFLRMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSTLAVNKKSS 122
Db 26 -----QRSGCLGSALAVNKKSS 42
QY 123 KFLPVGWSWMFSEYFLERSWAKDESTLKSGLQRLSDPPLFWLALFVEGTRFTQAKLL 182
Db 43 KFLPVGWSWMFSEYFLERSWAKDESTLKSGLQRLSDPPLFWLALFVEGTRFTQAKL 102
QY 183 AAOEYATSTGLPVRNVLIPRTKGFVSASHMSRFPVPAIYDVTVAI PKSSPAPTMRL 242
Db 103 AAOEYATSTGLPVRNVLIPRTKGFVSASHMSRFPVPAIYDVTVAI PKSSPAPTMRL 162
QY 243 GQPSVHVHVKHRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTSDQELQDTGP 302
Db 163 GQPSVHVHVKHRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTSDQELQDTGP 222
QY 303 IKSLVVISWACLAVAGSVKFLQWSLLSKWGVAFSAFLAVVATMALMOILIOFSQSE 362
Db 223 IKSLVVISWACLAVAGSVKFLQWSLLSKWGVAFSAFLAVVATMALMOILIOFSQSE 282
QY 363 NPAKIVPAKSN 374
Db 283 TPAKIVPAKPD 294

RESULT 8

Q93317

ID Q93317 PRELIMINARY; PRT; 311 AA.

AC Q93317;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE 1-acyl-sn-glycerol-3-phosphate acyltransferase.

OS Brassica napus (Rape).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=cv. jet neuf;
RA Brown A.P., Brough C.L., Kroon J.T., Slabas A.R.;
RT "Nucleotide sequence of a cDNA for a putative 1-acyl sn-glycerol-3-
RT phosphate acyltransferase from rape."
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z49860; CAA30019.1; -;
DR PIR; T07936; T07936.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002123; Acyltransferase.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SMO0563; PISC; 1.
DR DR POSITE; PS00038; HLH 1; 1.
KW Acyltransferase; transferase.
SQ SEQUENCE 311 AA; 34446 MW; C80FFEF97A144FBB CRC64;

Query Match 59.8%; Score 1156.5; DB 10; Length 311;
Best Local Similarity 61.4%; Pred. No. 8.8e-95;
Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;

QY 5 AAATVVPGLLFFASGLLVNLQIAICVYVVRPVSKSLYRINRVVAELLWLELVLDWM 64
DB 4 AAATVVPGLLFFISGLLVNLL----- 25

QY 65 AGVQVQIFTDHEIFRLMGKEHALVINHRSDIDMLVGVSAQPSGCLGSLTAVMKSSKF 124
DB 26 -----QSGGCLGALAVMKSSKF 44

QY 125 LPVIGSMWSEYFLERSWAKDESTLKSGIQRSLDPFPLFWALFVEGTRFTQAKLLAA 184
DB 45 LPVIGSMWSEYFLERNWAKDESTLKSGIQRSLDPFPLFWALFVEGTRFTQAKLLAA 104

QY 185 QEATSTGLPVRNVLIPRTKGFVSAVSHMRSTVPAIYDVTVAIPKSSPAPTMLRFLKQ 244
DB 105 QEAAASELVPVRNVLIPRTKGFVSAVSNMRSTVPAIYDVTVAIPKSSPAPTMLRFLKQ 164

QY 245 PSVVHVHIKHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTGRPI 304
DB 165 PSVVHVHIKCHSKMDLPSEDETAQWCRDQFVTKDALLDKHIAADTFAGQKEQNGRIK 224

QY 305 SLIVVISWACLIVAGSVKFLQWSLLSSWKGVAFAFGLAVVTALMQLLIQFSQSRSNP 364
DB 225 SLAVLSWACLITLGAMKFLHNSLFPSSWKGIALSALGLGIITLCMQLIRSSQSRSTP 284

QY 365 AKIVPAKSKN 374
DB 285 AKVAPAKPKD 294

RESULT 9
QYX9L2 PRELIMINARY; PRT; 237 AA.
ID QYX9L2
AC QYX9L2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1-acyl-glycerol-3-phosphate acyltransferase (fragment).
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. PH 82-2-2; TISSUE=Seed;
RA Li J.R., Wang F., Li Q.Z., Zhang X.S.;
RT "Gene isolation and expression of 1-acyl-glycerol-3-phosphate

acyltransferase.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF479037; AAP80656.1; -;
KW Acyltransferase; Transferase.
FT NON TER
SQ SEQUENCE 237 AA; 26693 MW; F4A164BDA47243A1 CRC64;

Query Match 43.6%; Score 844.5; DB 10; Length 237;
Best Local Similarity 74.3%; Pred. No. 4.1e-67;
Matches 162; Conservative 20; Mismatches 35; Indels 1; Gaps 1;

QY 86 ALVINSHRSDDMLVGVSAQPSGCLGSLTAVMKSSKFLPVIGSMWSEYFLERSWA 145
DB 3 ALLISNHRSDIDMLVGVSAQPSGCLGSLTAVMKSSKFLPVIGSMWSEYFLERSWA 62

QY 146 KDESTLKSIGIQRSLDPFPLFWALFVEGTRFTQAKLLAAQYATSTGLPVRNVLIPRTK 205
DB 63 KDESTLKSIGIQRSLDPFPLFWALFVEGTRFTQAKLLAAQYATSTGLPVRNVLIPRTK 122

QY 206 GFVSAVSHMRSTVPAIYDVTVAIPKSSPAPTMLRFLKQSPVHVHVKHLMKELPDTDE 265
DB 123 GFVSAVSHMRSTVPAIYDVTVAIPKSSPAPTMLRFLKQSPVHVHVKHLMKELPDTDE 182

QY 266 AVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTGRPI 303
DB 183 DSVKWCQDIFVAXDALLGQTYSNWSF-DXENIPXRP 219

RESULT 10
QYD517 PRELIMINARY; PRT; 376 AA.
ID QYD517
AC QYD517;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2003 (TrEMBLrel. 23, Last sequence update)
DE Adult male testis cDNA, RIKEN full-length enriched library,
DE clone:4930526114 product:1-acylglycerol-3-phosphate O-acyltransferase
DE 3, full insert sequence (1-acylglycerol-3-phosphate-gamma)
DE (EC 2.3.1.51) (1-acylglycerol-3-phosphate O-acyltransferase 3).
GN AGPAT3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head, Liver, and Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;

Db 196 GLPPLKYLHLLPRTKGTFTAVQCLRGTVAAIYDVTLNF-RGNKNPSSLLGILYKGYEADWC 254

QY 252 IKRHLMKELPDDEAVACWCRDIFVAKDALLDKHMAEGTFSDQELQDGRPKISLLVVIS 311

Db 255 VRRFPLEDPADETSAAQWLHLYQKDALQEMYKQGVFPQGPAPRRP-WTLNLFIC 313

QY 312 WACLIVAGSVKFLQWSLLSSWKGVAFAFGLAVVTAL 349

Db 314 WATILL-----SPFSFVLGVAFSGSPLLILTF 342

RESULT 12

Q7ZYII PRELIMINARY; PRT; 376 AA.

AC Q7ZYII

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Similar to 1-acylglycerol-3-phosphate O-acyltransferase 3.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Klein S., Strausberg R.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC043776; AHA43776.1; -.

DR GO; GO:0008415; F:acyltransferase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002123; Acyltransferase.

DR Pfam; PF01553; Acyltransferase; 1.

DR SMART; SMC0563; Pfam; 1.

KW Transferase; Acyltransferase.

SQ SEQUENCE 376 AA; 43685 MW; 52ADFCEBBB460D CRC64;

Query Match 30.8%; Score 595.5; DB 13; Length 376;

Best Local Similarity 34.4%; Pred. No. 1.2e-44;

Matches 118; Conservative 79; Mismatches 125; Indels 21; Gaps 5;

QY 12 LGLLFASGLVNLICAVVVRPVSKSYLRINEVVAELMLLEVLMLDWAGVKVQI 71

Db 17 IGVFVVSGLINFLQ-LCTPLWGIKPLIRINCMEAYLLWSQLVMLEWNSGTQCTL 75

QY 72 FTDHETFRLMGKEHALVSNHRSDDILVGVWSAQRSGCLGSTLAVMKSSKFLPVIGWS 131

Db 76 FSDQKIDHFGKEHVIILNHNHYEIDFLCGWTWCERYGLGSKVLAKKELLMVPLIGWT 135

QY 132 MWSEVILFLERSWAKDESLKSGIQRLSDPLFPFLALFVEGTFTQAKLLAAQEVATST 191

Db 136 WYFLEIVFCRKEEDRDVTIOGLKDLRDYPEYMWFLLYCEGTRFTETKHKISMEVADCK 195

QY 192 GLPVPNRNLIPRTKGFVSAYSHMRSFVPAIYDVTVTAIPKSSPAPTMLRLFKGQPSVVVHV 251

Db 196 GLARLKHLLPRTGFTTAVQCLRGTVAAIYDVTLSF-RGNKNPSSLLGILYKGYEADWC 254

QY 252 IKRHLMKELPDDEAVACWCRDIFVAKDALLDKHMAEGTFSDQELQDGRPKISLLVVIS 311

Db 255 VRRFPLEEDPEKEAAWHLHLYQKDALQEQYIQEGTFPGTQIVPPRRP----- 305

QY 312 WACLIVAGSVKFLQWSLLSSWKGVAFAFGLAVVTALMQILI 354

Db 306 WTLI-----NFLWAILLS-----PLFSPAIGIFASGSPLLI 338

RESULT 13

Q9VV51 PRELIMINARY; PRT; 396 AA.

AC Q9VV51; Q9VV50;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

CG4729 protein (REI0780p).

QY CG4729

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).

RC STRAIN=Berkely;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazei R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Nikifor B.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jaisl M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleeb J.M.,

RA Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,

RA Reaier K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

RA Miranda A., Mungall C.J., Nunoo J., Pacleeb J., Paragas V., Park S.,

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.;

RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

RL -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Long;

CC IsoId=Q9VV51-1; Sequence=Displayed;

CC Name=Short;

CC IsoId=Q9VV51-2; Sequence=VSP_050280;

DR EMBL; AE003527; AAF49471.1; -.

DR EMBL; AE003527; AAF49472.1; -.

DR EMBL; BT001546; AAN71301.1; -.

DR FlyBase; FBGN0036623; CG4729.

DR GO; GO:0008415; F:acyltransferase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

Search completed: July 7, 2004, 13:41:18
Job time : 48 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 13:33:37 ; Search time 18 Seconds
(without alignments)
1090.590 Million cell updates/sec

Title: US-09-914-098-56

Perfect score: 1935

Sequence: 1 MALAAAVVPLGLFFASG.....QSERNSPAKIVPAKSKNGS 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	628	32.5	376	1 PLCC_HUMAN	Q9nrz7 homo sapien
2	554.5	28.7	378	1 PLCC_HUMAN	Q9nrz5 homo sapien
3	551.5	28.7	378	1 PLCC_HUMAN	Q9nrz5 homo sapien
4	304	15.7	364	1 PLCE_MOUSE	Q9nuq2 homo sapien
5	303	15.7	365	1 PLCE_MOUSE	Q9nuq2 homo sapien
6	271	14.0	397	1 YB2 YEAST	P38226 saccharomyc
7	247	12.8	396	1 YB2 YEAST	Q12185 saccharomyc
8	186.5	9.6	370	1 Y205_HUMAN	Q92604 homo sapien
9	148	7.6	330	1 YH9_ECOLI	P32129 escherichia
10	124.5	6.4	391	1 Y773_CABEL	Q11087 caenorhabdi
11	121	6.3	303	1 PLSC_YEAST	P33333 saccharomyc
12	120	6.2	245	1 PLSC_ECOLI	P26647 escherichia
13	120	6.2	245	1 PLSC_SALTY	P26974 salmonella
14	118.5	6.1	281	1 PLSC_LIMAL	Q42868 limnanthes
15	118.5	6.1	281	1 PLSC_LIMDO	Q42870 limnanthes
16	115.5	6.0	240	1 PLSC_HAEIN	P44848 haemophilus
17	109	5.6	278	1 PLCE_HUMAN	Q15120 homo sapien
18	105	5.4	282	1 PLC2_CABEL	Q22267 caenorhabdi
19	100.5	5.2	722	1 GRE4_CHLPN	Q92754 chlamydia p
20	100	5.2	391	1 PER_DROIN	P91613 drosophila
21	98	5.1	396	1 PER_DROPU	P91697 drosophila
22	98	5.1	386	1 PER_DROPV	P91698 drosophila
23	97	5.0	395	1 PER_DROTP	P92203 drosophila
24	96	5.0	390	1 PER_DROTP	P91716 drosophila
25	95.5	4.9	283	1 PLCA_HUMAN	Q99943 h 1-acyl-sn
26	95	4.9	308	1 PLSC_COCNU	Q42670 cocos nucif
27	95	4.9	1093	1 PER_DROWI	Q03297 drosophila
28	93	4.8	285	1 PLCA_MOUSE	Q35083 mus musculu
29	93	4.8	428	1 YXIO_BACSU	P42306 bacillus su
30	92	4.8	397	1 NXFS_HUMAN	Q9h1b4 homo sapien
31	91.5	4.7	384	1 UT1_MOUSE	Q8vh10 mus musculu
32	91.5	4.7	844	1 RRPO_IPNVS	P22174 infectious
33	90	4.7	1679	1 YMF9_YEAST	Q04958 saccharomyc

34 90 4.7 2103 1 RRPL_UUK P33453 ukunieni v
35 89.5 4.6 718 1 PLSB_CABEL Q2949 caenorhabdi
36 89 4.6 262 1 PLCL_CABEL Q3841 caenorhabdi
37 89 4.6 2832 1 NDVB_RHIME P20471 rhizobium m
38 88.5 4.6 804 1 SYFB_BRUSU Q8fxx4 bruceella su
39 88.5 4.6 920 1 MML7_MYCTU P96289 mycobacteri
40 88.5 4.5 1099 1 CYA7_MOUSE P51829 mus musculu
41 88 4.5 973 1 Y064_MYCTU O53609 mycobacteri
42 88 4.5 979 1 Y065_MYCHO Q9u2x8 mycobacteri
43 87.5 4.5 804 1 SYFB_BRUSU Q8ye74 bruceella me
44 87.5 4.5 857 1 I2C1_MOUSE Q8cjl1 mus musculu
45 87 4.5 336 1 PYRD_VIBUO Q8d9g5 vibrio vuln

ALIGNMENTS

RESULT 1
PLCC_HUMAN
ID PLCC_HUMAN STANDARD; PRT; 376 AA.
AC Q9NRZ7; Q9NRZ6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1-acyl-sn-glycerol-3-phosphate acyltransferase gamma (EC 2.3.1.51) (1-
AGP acyltransferase 3) (1-AGPAT 3) (lysophosphatidic acid
DE acyltransferase-gamma) (LPAAT-gamma) (1-acylglycerol-3-phosphate O-
DE acyltransferase 3).
GN AGPAT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]__taxid:9606;
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA-1 AND GAMMA-2).
RA Leung D.W.;
RT "Structure and functions of lysophosphatidic acid acyltransferases.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Hase T.,
RA Shimizu N.;
RT "Isolation of a novel gene encoding 1-acylglycerol-3-phosphate
RT O-acyltransferase 3 (AGPAT3) from the human chromosome 21q22.3.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RC Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
CC -!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic
acid by incorporating acyl moiety at the 2 position (By
similarity).
CC

Best Local Similarity 31.6%; Pred. No. 5.8e-41;
Matches 114; Conservative 94; Mismatches 148; Indels 5; Gaps 4;

QY 15 LFFASGLVNLQIAICVYVVRVPSKSLYRRINRVVAELLMLELVMLIDMWAGVKVQIFTD 74
Db 20 VFASGLIINTIQ-LFTLLWLPINKQLFRKINARLCVCVSSQLVLMLEWMSGTECTIYTD 78
QY 75 HETFLMKGHALVSNHRSIDWLVGVSAQSCGLSTLAVMKSSKFLPVIGSMWF 134
Db 79 PRAYLKYGKNAIVNLNKHFEIDFCGWSLSEFGLGSKVLAKKELAYVPIIGMWYF 138
QY 135 SEYLFERSWAKDESLKSGIQRSLDFPLFWLALFVEGTRFTQAKLLAAQEVATSTGLP 194
Db 139 TEWVFCRSKWEQDRKTVATSLQHLRDYPEKYFLLIHCEGTRFTEKKHHSIQVAKAGLP 198
QY 195 VPRNVLIPRTKGFVSAVSHMRSPFALYDVTVAIKSSPAPMLRLFKGQSPVHVHILKR 254
Db 199 RLKXHLPRTKGFAITVSRNWSAVYDCTLNF-RNNENPTLLGVNLGKKYHADLYVR 257
QY 255 HLMKELPDTDEAVACQCRDIFVAKDALLDKHMAEGTFSDQELQDTGRIKSLILVVISWAC 314
Db 258 IPEIDPEDDSCSAWLHKLYQEKAFQBEYRTGTFPTVPVPRRP-WTLVNLWLFAS 316
QY 315 LVVAGSVKFLQWSLLSSWKGVAFAFGLAVVTLAQILIQFSQSRNPAPKIVPAKSN 374
Db 317 LVLYPFFQEL--VSMIRSGSLTLASFILVFFVAVGVVRMIGVTEIDKGSAYGNSDSKQ 374
QY 375 K 375
Db 375 K 375

RESULT 3
PLCD RAT STANDARD; PRT; 378 AA.

AC Q24SI;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 1-acyl-sn-glycerol-3-phosphate acyltransferase delta (BC 2.3.1.51) (1-
AGP acyltransferase 4) (1-AGPAT 4) (Lysophosphatidic acid
acyltransferase-delta) (LPAAT-delta) (1-acylglycerol-3-phosphate O-
acyltransferase 4).
DE AGPAT4.
GN Rattus norvegicus (Rat).
OS Rattus norvegicus mRNA for lysophosphatidic acid
Li W., Suzuki T.;
RT "Rattus norvegicus delta, complete cds."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic
acid by incorporating acyl moiety at the 2 position (By
similarity).
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate =
CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
CC -!- PATHWAY: De novo phospholipid biosynthesis; second step.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
acyltransferase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB067572; BAB62290.1; -

DR InterPro; IPR002123; Acyltransferase.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; PlcC; 1.
KW Phospholipid biosynthesis; Transferase; Acyltransferase;
FT TRANSMEM 11
FT TRANSMEM 31
FT TRANSMEM 125
FT TRANSMEM 145
FT TRANSMEM 307
FT TRANSMEM 327
FT TRANSMEM 338
FT TRANSMEM 358
SQ SEQUENCE 378 AA; 43794 MW; 389AA01B7327AE2B CRC64;

Query Match 28.5%; Score 551.5; DB 1; Length 378;
Best Local Similarity 33.7%; Pred. No. 1.1e-40;
Matches 114; Conservative 81; Mismatches 138; Indels 5; Gaps 4;

QY 15 LFFASGLVNLQIAICVYVVRVPSKSLYRRINRVVAELLMLELVMLIDMWAGVKVQIFTD 74
Db 20 VFASGLIINTIQ-LFTLLWLPINKQLFRKINARLCVCVSSQLVLMLEWMSGTECTIYTD 78
QY 75 HETFLMKGHALVSNHRSIDWLVGVSAQSCGLSTLAVMKSSKFLPVIGSMWF 134
Db 79 PRAYLKYGKNAIVNLNKHFEIDFCGWSLSEFGLGSKVLAKKELAYVPIIGMWYF 138
QY 135 SEYLFERSWAKDESLKSGIQRSLDFPLFWLALFVEGTRFTQAKLLAAQEVATSTGLP 194
Db 139 TEWVFCRSKWEQDRKTVATSLQHLRDYPEKYFLLIHCEGTRFTEKKHHSIQVAKAGLP 198
QY 195 VPRNVLIPRTKGFVSAVSHMRSPFALYDVTVAIKSSPAPMLRLFKGQSPVHVHILKR 254
Db 199 RLKXHLPRTKGFAITVSRNWSAVYDCTLNF-RNNENPTLLGVNLGKKYHADLYVR 257
QY 255 HLMKELPDTDEAVACQCRDIFVAKDALLDKHMAEGTFSDQELQDTGRIKSLILVVISWAC 314
Db 258 IPEIDPEDDSCSAWLHKLYQEKAFQBEYRTGTFPTVPVPRRP-WTLVNLWLFAS 316
QY 315 LVVAGSVKFLQWSLLSSWKGVAFAFGLAVVTLAQILIQFSQSRNPAPKIVPAKSN 374
Db 317 LVLYPFFQEL--VSMIRSGSLTLASFILVFFVAVGVVRMIGVTEIDKGSAYGNSDSKQ 374

RESULT 4
ID PLCD HUMAN STANDARD; PRT; 364 AA.
AC Q9NUQ2; O81Z47; Q9BQ4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon (EC 2.3.1.51)
DE (1-AGP acyltransferase 5) (1-AGPAT 5) (Lysophosphatidic acid
acyltransferase-epsilon) (LPAAT-epsilon) (1-acylglycerol-3-phosphate
O-acyltransferase 5).
DE AGPAT5.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Leung D.W.;
RT "Cloning and expression of LPAAT-epsilon."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC [2]
RP SEQUENCE FROM N.A.
RA Cohen D., Chumakov I., Blumenfeld M., Bougueleret L.;
RL Patent number WO9932644, 01-JUL-1999.
RP [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Cassenhuber J., Glassl S.,
RA Ansgorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Dueterhoeft A., Beyer A., Koehler K., Strack N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,

Query Match	15.7%	Score 304.7	DB 1	Length 364
Rest Local Similarity	28.8%	Pred. No. 4.5e-19		
Matches 76	Conservative 65	Mismatches 105	Indels 18	Gaps 7
QY	57	LVMLDWMAGVKVOIFDTHETFLRMGKEHALVSNHRSIDWLGVWVSAQSRGCLGSLIA	116	
Db	62	VLFPPENTYGOVILLYGDLP----	117	
QY	117	VMKSSKSLPVGHSWMFSEY--LFLERSWAKDESTLKSIGQRLSDFFLPFWLALFVEGT	174	
Db	118	VUKEGLKWLPLYG--CFYAGHGGLYKRSAKFNEKMRNKLOSYYDACTPFWYLVFPEGT	175	
QY	175	RFT--QAKLL-AAQEVATSTGLFVPRNVLIPRTKGFVSASHMRSFVPAIDVTVVAIP--	229	
Db	176	RYNPEQTQVLSASQAPAAQGLAVLKHVLTFRPKATHVAFDCWKYLDALYDVTVVYEGK	235	
QY	230	----KSSPAPFMLELFGQSVVHVHVKHLMKELPDDTEAVAQWCRDIFVAKALDDKH	288	
Db	236	DGQGRRESPTMTFLOCEPKIHIIHIDRKDVPEOEQEHRRVRLHFRFEIKQMLIE-	294	
QY	286	MAEGTFSQELQDTGRPIKSLVVV	309	
Db	295	FYSPDPERRKFFPGKSVNSKLSI	318	

RESULT 5

PLCE MOUSE	STANDARD;	PRT;	365 AA.
ID	Q9DLE8; Q8BG61; Q8CGN6;		
AC	28-FEB-2003 (Rel. 41, Created)		
DT	10-OCT-2003 (Rel. 42, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon (BC 2.3.1.51)		
DE	(1-AGP acyltransferase 5) (1-AGPAT 5) (Lysophosphatidic acid		
DE	acyltransferase-epsilon) (LPAAT-epsilon) (1-acylglycerol-3-phosphate		
DE	O-acyltransferase 5).		
GN	AGPAT5		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TaxID=10090;			
OK			
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=NMRI;		
RA	Lu B., Jiang Y.J., Chan M., Choy P.C.;		
RT	"Identification and characterization of 1-acylglycerolphosphate		
RT	acyltransferase-epsilon.";		
RL	Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J, and NOD; TISSUE=Cerebellum, Embryo, and Spleen;		
RC	MEDLINE=22354683; PubMed=12466851;		
RX	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,		
RA	Nakaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,		
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,		
RA	Baldacelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,		
RA	Schriml L.M., Knappin A., Matsuda H., Batalov S., Beisel K.W.,		
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,		
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,		
RA	Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,		
RA	Grummond S., Gustinctsch S., Hirokawa N., Jackson I.J., Jarvis E.D.,		
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,		
RA	Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,		
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,		
RA	Nagashtima T., Numata K., Okido T., Pavan W.J., Perteza G., Pesole G.,		
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,		
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,		
RA	Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,		
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,		
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,		
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,		
RA	Yuan Z., Zavalan M., Zhu Y., Zimmer C., Zimnicki B., Zuvatzki M.,		

Qy	41	LYRINRVVAELLWLEVLMLDWDAGVKYQIETDHTFRLMGKHEALVISNHRSDIDWLVI	100
Dp	46	LYQVDRDLRCVTQNMVVLPFFENYTQGLLLYGDLP----	101
Qy	101	GWSAQSRSGCIGSTLAVMKKSSXFLVIGWSYWFSEY--LFLEERSMAKDSTLKSGIQRL	158
Dp	102	ADMLAARQDALGHVRVYLKDKLKWLPYGF--VFACHGGIYVKRSAKFNDEMRSLQSY	159
Qy	159	SDFELPFWLALFVEGTFR--TQAKLI-ARQEVATSTGLVPNNVLIPTKGFSVASVSHWR	215
Dp	160	VNAGTPMYLVIFPEGTRYNAITYTKLLSASCAFAAORGLAVLKHVLTPIKATHVAFDSMK	219
Qy	216	SFVPAIVDVTVTAIP-----KSPAPTMLRLFQKQPSVHVHIIKRHLMKELPDTDEAVA	268
Dp	220	SHLDIAIVDVTVVEGNEKSGSKYNPPSMTEFLCKQCPKLHIHFDRIDNRNEVPEQEHHM	279
Qy	269	QWCQRDIIFVAKDALL 282	
Dp	280	KWLHERFEIKDRLL 293	
 RESULT 6 ID YBP2 YEAST STANDARD; PRT; 397 AA.			
DT	01-OCT-1994	(Rel. 30, Created)	
DT	01-OCT-1994	(Rel. 30, Last sequence update)	
DT	16-OCT-2001	(Rel. 40, Last annotation update)	
DE	Hypothetical 45.5 kDa protein in PAT1-TCM62 intergenic region.		
GN	YBR042C OR YBR0412.		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
CC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.		
RN	NCBI_TaxID=4932;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RA	STRAIN=S288c;		
RC	Andre B., Czepluch C., Hein C., Jauniaux J.-C., Urrestarazu A.,		
RA	Visiers S.;		
RL	Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).		
CC	-!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate		
CC	acyltransferase family.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	or send an email to license@sb-sib.ch).		
CC	EMBL; Z35911; CAAB4984.1; --		
DR	PIR; S45900; S45900.		
DR	GermOnline; 138585; --		
DR	SGD; S0000246; YBR042C.		
DR	InterPro; IPR002123; Acyltransferase.		
DR	Ffam; PF01553; Acyltransferase; 1.		
DR	SMART; SM00563; Pfsc; 1.		
KW	Hypothetical protein; Phospholipid biosynthesis; Transferase;		
KW	Acyltransferase; Transmembrane.		
FT	TRANSMEM 13 33 POTENTIAL.		
FT	TRANSMEM 58 78 POTENTIAL.		
FT	TRANSMEM 118 138 POTENTIAL.		
FT	TRANSMEM 377 397 POTENTIAL.		
SQ	SEQUENCE 397 AA; 45515 MW; 04CADD1247D9BA8 CRC64;		
 Query Match 14.0%; Score 271; DB 1; Length 397; Best Local Similarity 24.6%; Pred. No. 3.9e-16; Matches 87; Conservative 72; Mismatches 122; Indels 72; Gaps 13			
Qy	8	VVVP-LGLIFFASGLLVNLICAIQCVVVRPVSKSLY-----RRINRVVAELLWLEVL-V	59

Cy 8 VVVP-LGLIFASGILLVNLIQAICVVVRPVSKSLY-----PRINRVVAELLNLELV-W 59
||||| : |||| | : |||| : |||| : ||||
Matches 87; Conservative 72; Mismatches 122; Indels 72; Gaps 13

Best Local Similarity 24.0%, Field NO. 3-36 187

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwold J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
CC acyltransferase family.
CC -----
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CC -----
CC EMBL; D86960; BAA13196.1; -;
DR EMBL; BC034621; AAH34621.1; -;
DR InterPro; IPR002123; Acyltransferase.
DR SMART; SM00563; Pfam; 1.
KW Hypothetical protein; Phospholipid biosynthesis; Transferase;
KW Acyltransferase; Transmembrane.
FT TRANSMEM 22 42
FT TRANSMEM 342 362 POTENTIAL.
SQ SEQUENCE 370 AA; 43089 MW; 93498544EA651541 CRC64;
Query Match 9.6%; Score 186.5; DB 1; Length 370;
Best Local Similarity 23.6%; Pred. No. 8.9e-09;
Matches 78; Conservative 58; Mismatches 117; Indels 77; Gaps 16;
QY 14 LPPFASGLLVNLI--QAICYVVV---RPVSKSLYRRNRVVAE-LIMLELVLLIDMWA 65
DB 19 LMFAPVNNVNVVAISYCYVILLOPLVLSKRFWYEGIMYKLLGWASW--GWYA 76
QY 66 GVKVQIFTDETRLMGKHEALVISNRSDIDMLGVNSAQSGCLGSLTAVNKKSSKPL 125
DB 77 GYTVMEW--GEDIKAVSKDEAVMLNVHQATGDVCTLMMLQDKGL----- 119
QY 126 PVIGNSWSEYFLERSA-----KDES--TLKSGIQ---RLSDPPL 163
DB 120 -VVAQWMLMDHIFKTYNTGIVSLVHGDFPIROGRSYRQQLLLKHLENNYRDRK- 177
QY 164 PFWLALFVEGTRFTQAKLAAQYATSTGLVPRNVLIPIR--TKGFVSA-VSHMRSFVP 219
DB 178 --NIVLPEEG-GFLRKRRSTSQAFKKNLPLFTNTVLRSGATKIILNALVAQKNGSP 234
QY 220 A-----IDYTVVAIPKSSP--APTMLRFLKGPSVWVHHKRLMKELP 261
DB 235 AGGDAKELDSKSLGQLWIDTTIAPKAEFIDITQWILGYR-KPTVTHVHYRFFIKQVP 293
QY 262 DTDEAVAQWCRDIFVAKDALLDKHMAEGTF 291
DB 294 LETDDLTWLYQRFVEKEDLLSHFYETGAF 323
RESULT 9
ID YIHG_ECOLI STANDARD; PRT; 310 AA.
AC P32129;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yihg.
GN YIHG OR B3862.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;

RN SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RC MEDLINE=93347969; PubMed=8346018;
RX Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes";
RL Nucleic Acids Res. 21:3391-3398 (1993).
CC -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
CC acyltransferase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L19201; AAB02997.1; -;
DR EMBL; AE000461; AAC76860.1; -;
DR PIR; S40808; S40808.
DR EcoGene; EGI1833; yihg.
DR InterPro; IPR002123; Acyltransferase.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; Pfam; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 310 AA; 36289 MW; 9F8E3F52EB0B185E CRC64;
Query Match 7.6%; Score 148; DB 1; Length 310;
Best Local Similarity 21.6%; Pred. No. 1.6e-05;
Matches 71; Conservative 58; Mismatches 115; Indels 84; Gaps 14;
QY 6 AAVVPVGLLFFASGLLVNLIQAICYV--VVRPVSKSL-----YRRNRVVAELLWLEL 57
DB 15 AAITLLLSI-----VLTILVTIFCSVPILLAGIVKLLLPVPIVWRKVSRCDFDMYC-- 66
QY 58 VMLDWMAGVKVQIOTD-----HETFLMGKHEALVISNRSDIDMLGVNSAQSGC 110
DB 67 -----WCEGLAVLHLNPHIQWVHGLEGSKKQWYLLICNHRSWADIVLCVLFK-- 119
QY 111 LGSTLAVNKKSKFLPVIGNSWSEYFLER-----SWAKDESTLKSIGIQRLS 159
DB 120 IPNKKYFLKQALVAVPFLGLACWSLDMFPMKRYSAVLLRHPERRGKDVETTRSCCK- 177
QY 160 DPPL-PFWLALFVEGTRFTQAKLAAQYATSTGLVPRNVLIPIRTKGFVSAVSHMRSFV 218
DB 178 -FRLHPTTIVNFVSGSRFTQEK--HQOTHSTF-----QNLLPPKAAAGIAMLNVLGKQF 228
QY 219 PAIDYTVVAIPKSSPAPTMLRFLKGPSVWVHHI-----KRLMKKE 259
DB 229 DKLNLVILCYPDNNRQP-FFDNLGSKLTRIVVHVHDLQPIADLHGDINDKSFTRHQ-- 285
QY 260 LPDTDEAVAQWCRDIFVAKDALLDKHMA 287
DB 286 -----QWLNSLWQEKDRLLTSLMS 304
RESULT 10
ID Y173_CAEEL STANDARD; PRT; 391 AA.
AC Q11087;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 44.7 kDa protein COIC10.3 in chromosome X.
GN COIC10.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1] SEQUENCE FROM N.A.

100 WIPFPGQLYWLITGLNLLDRNRRTKAKHTTAIEVVNVHFKKRISIW--MPPEGTR-----150

183 AAQEVATSTGLPVRNVLIIRTKGVSVAVSHMRSFDPALYDVTVAIKSSPAPTMLRLEK 242

10CT-2003-----SRG-----RGLLPKPTGAFHAATA---AGVPFI---PVCVSTTSKNINLRH 193

151 -----SRG-----RGLLPKPTGAFHAATA---AGVPFI---PVCVSTTSKNINLRH 193

243 GQPSVVVHVKIRHLMKELPTD-----EAVAQWCRDIFVAKDALLDKHMAE 288

194 GLV-----IVEMLPIDVSQYKQDOVRELAHCRSIMEQKIAELDKVAE 238

RESULT 13

PLSC SALTY STANDARD; PRT; 245 AA.

AC P26974;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 10-OCT-2003 (Rel. 43, Last annotation update)

DE 1-acyl-sn-glycerol-3-phosphate acyltransferase [EC 2.3.1.51] (1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase) (LPAAT).

DE DE

GN PLSC OR PARF OR STM3173 OR STY3350 OR T3094.

OS Salmonella typhimurium, and

OS Salmonella typhi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=602, 601;

RN [1]_TaxID=602, 601;

RN SEQUENCE FROM N.A.

RC SPECIES=S.typhimurium; STRAIN=LT2;

RC MEDLINE=92089025; PubMed=1751451;

RX Luttiger A.L., Springer A.L., Schmid M.B.;

RT "A cluster of genes that affects nucleoid segregation in Salmonella typhimurium.";

RT New Biol. 3:687-697(1991).

RL [2]

RN SEQUENCE FROM N.A.

RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;

RC MEDLINE=21534948; PubMed=11677609;

RX McCelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

RA "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";

RA Nature 413:852-856(2001).

RL [3]

RN SEQUENCE OF 236-245 FROM N.A.

RC SPECIES=S.typhimurium; STRAIN=LT2;

RC Cong J., Schmid M.B.;

RA Submitted (Apr-1994) to the EMBL/GenBank/DBJ databases.

RL [4]

RN SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=CT118;

RC MEDLINE=21534947; PubMed=11677608;

RX Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M., Baker S., Basham D., Brooks K., Chillingworth T., Connor P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;

RA "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";

RA Nature 413:848-852(2001).

RL [5]

RN SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=TY2 / ATCC 700931;

RC MEDLINE=22531367; PubMed=12644504;

RX Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;

DE 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP
DE acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
DE (LPAAT).
GN PLSC.
OS Limnanthes douglasii (Douglas's meadowfoam).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Limnanthaceae; Limnanthes.
OX NCBI_TaxID=28973;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96028122; PubMed=7588719;
RX MEDLINE=96046746; PubMed=7579178;
RA Brown A.P., Brough C.L., Kroon J., Slabas A.R.;
RT "Identification of a cDNA that encodes a 1-acyl-sn-glycerol-3-
RT phosphate acyltransferase from Limnanthes douglasii.";
RL Plant Mol. Biol. 29:267-278(1995).
CC -!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic
CC acid by incorporating acyl moiety at the 2 position. This enzyme
CC uses erucyl-CoA as an acyl donor.
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate =
CC CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
CC -!- PATHWAY: de novo phospholipid biosynthesis; second step.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
CC acyltransferase family.
CC -----
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CC -----
CC EMBL; X83266; CAAS8239.1; -;
CC EMBL; Z46836; CAAS86877.1; -;
CC PIR; S60477; S60477.
CC InterPro; IPR002123; Acyltransferase.
CC InterPro; IPR004552; AGP acyltrn.
CC Pfam; PF01553; Acyltransferase; 1.
CC SMART; SM00563; PlsC; 1
CC TIGRFAMs; TIGR00530; AGP-acyltn; 1.
CC KW Phospholipid biosynthesis; Transferase; Acyltransferase;
KW Transmembrane.
FT TRANSMEM 40 60 POTENTIAL.
FT TRANSMEM 71 91 POTENTIAL.
FT TRANSMEM 110 130 POTENTIAL.
FT CONFLICT 46 46 I -> V (IN REF. 2).
FT CONFLICT 188 188 R -> G (IN REF. 2).
FT CONFLICT 262 262 V -> I (IN REF. 2).
FT CONFLICT 281 281 N -> K (IN REF. 2).
SQ SEQUENCE 281 AA; 31716 MW; 9C880BD9E492EE2A CRC64;

Query Match 6.1%; Score 118.5; DB 1; Length 281;
Best Local Similarity 21.7%; Pred. No. 0.0055;
Matches 56; Conservative 46; Mismatches 79; Indels 77; Gaps 12;
QY 29 ICYVVRPVSKLYRINRVAEELW-----LELVW-----LIDWAG 66
DB 42 VCFAIV-----LITAVAGLIMVLLPWPYMRIRGLNLYGHIGGLVIWYG 88
QY 67 VKVQITDHTFRLMKEHALVINSRSDID-WLVCWVSAQRSGCLGSLAVWKKSKFL 125
DB 89 IPIKQGSHT-----KKRAIYISNHASPIDAFFVWMLAP-----IG-TVGAKKEVIWY 137

QY 126 PVIGSMWTFSEYLFILERS-WAKDESTLKSIGIORLSDFPLPFWLALFVEGTRFTQAKLAA 184
DB 138 PLLGQLYTLAHHIRIDRSNPAAIQSMKEAVRVIETKNLS--LIMFPEGTRSDGRLLP 195
QY 185 QE-----YATSTGLPVRNVL-----IPRTKGFVS-----AVSHVRSF 217
DB 196 KKGFEVHLALQSHLPVIFPMILTGTHLAWRGTFRVREPVTIVKYLPPINTDDMTVDKIDDY 255
QY 218 VPAIYDVTVVAIPKSSPAP 235
DB 256 VKMIHDVYVYNLFPASQKP 273
Search completed: July 7, 2004, 13:40:19
Job time : 20 secs

1-acyl-sn-glycerol
1-acyl-sn-glycerol
1-acylglycerol-3-p
hypothetical prote
probable acyltrans
probable 1-acygly
1-acyl-sn-glycerol
1-acylglycerol-3-p
1-acylglycerol-3-p
hypothetical prote
transcription elon
2-acylglycerophosp
probable 1-acygly
1-acylglycerol-3-p
conserved hypothet

30 115 5.9 245 2 F85961
31 115 5.9 245 2 F91116
32 111 5.7 243 2 AC0083
33 108.5 5.6 241 2 G97788
34 108 5.6 257 2 A83645
35 106.5 5.5 243 2 B71706
36 105 5.4 247 2 G81013
37 105 5.4 282 2 T24610
38 104.5 5.4 247 2 A81957
39 101.5 5.2 247 2 G72223
40 100.5 5.2 722 2 B86583
41 100.5 5.2 722 2 C72040
42 97.5 5.0 211 2 E70476
43 93.5 4.8 261 2 C82067
44 93 4.8 285 2 JC5639
45 93 4.8 428 2 B70078

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: July 7, 2004, 13:37:33 ; Search time 21 Seconds
(without alignments)
1726.867 Million cell updates/sec
Title: US-09-914-098-56
Perfect score: 1935
Sequence: 1 MAIAAAVVVPLGLFFASG.....QSERNPAPIVPAKSKNGS 377
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
S60478
Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase - Limnanthes douglasii
C:Species: Limnanthes douglasii
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C:Accession: S60478
R:Brown, A.P.; Brough, C.L.; Kroon, J.T.M.; Slabas, A.R.
Plant Mol. Biol. 29, 267-278, 1995
A:Title: Identification of a cDNA that encodes a 1-acyl-sn-glycerol-3-phosphate acyltra
A:Reference number: S60477; MUID:96046746; PMID:7579178
A:Accession: S60478
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-377 <BRO>
A:Cross-references: EMBL:Z48730; NID:G1067137; PIDN:CAA88620.1; PID:G1067138
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
C:Superfamily: probable membrane protein YBR042C

Query Match 78.5%; Score 1519; DB 2; Length 377;
Best Local Similarity 77.0%; Pred. No. 1.5e-124; Indels 0; Gaps 0;
Matches 282; Conservative 43; Mismatches 41;
QY 1 MAIAAAVVVPLGLFFASGLLVNLIQACVWVVRPVSKSLYRINRVVAELMLVWL 60
DB 1 MAIPAAAFIVPISLLFFNSGLVNFQAVFYVLRPIKDYRINTLVAEMLVWL 60
QY 61 IDWAGVKVQIPTDHTETFLMGKEHALVINSRSDIDWLVGVNSAQRSGCLSTLAVMKK 120
DB 61 IDWAGVKVQIYTDTSFRLMGKEHALICNHRSDIDWLVGVNSAQRSGCLSSIAVMKK 120
QY 121 SKKFLPVIGSWWRFSEYLFERNWAKDENTLKSGLQRLNDFPKFWLALFVEGTFTKAX 180
DB 121 SKKFLPVIGSWWRFSEYLFERNWAKDENTLKSGLQRLNDFPKFWLALFVEGTFTKAX 180
QY 181 LLAQAEYATSTGLPVRNVLIPTKGFVSASHMFSFVPAIYDVTVTAIPKSSPAPTMRL 240
DB 181 LLAQAEYAAAGLPVRNVLIPTKGFVSASHMFSFVPAIYDLTAIPAIPKTEQPTMLRL 240
QY 241 FKGQPSVVVHHIKRHLMKELPDTDEAVAQWCPDIFVAKDALLDKHMAEGRSDQLQDTG 300
DB 241 FRKGSVVVHHIKRHLMKDLPKTDGVAQWCKDQFISKDALLDKHVAEDFTFSGLEVDIG 300
QY 301 RPTKSLVWISWACLVVAGSVKFLQWSSLLSSWKGVSFAFGLVAVVTALMQILIFSQSE 360
DB 301 RPKMSLVVWVSWVCLLCGLVAFQWSSLLSSWKGVSFAFGLVAVVTALMQILIFSQSE 360
QY 361 RNPAPK 366
DB 361 HSTPAK 366

RESULT 2

Result No.	Score	Query Match %	Length	DB ID	Description
1	1519	78.5	377	S60478	probable 1-acyl-sn
2	1450.5	75.0	374	S52645	probable 1-acyl-gl
3	1277	66.0	376	D96550	hypothetical prote
4	1161.5	60.0	310	T06755	probable glycerol-
5	1156.5	59.8	311	T07936	probable glycerol-
6	414	21.4	393	B96780	hypothetical prote
7	310.5	16.0	350	T40466	probable acetyltra
8	287	14.8	344	T31913	hypothetical prote
9	271	14.0	397	S45900	probable membrane
10	269	13.9	918	T34057	hypothetical prote
11	250	12.9	439	T22689	hypothetical prote
12	247	12.8	395	S54641	probable membrane
13	240.5	12.4	523	T25988	hypothetical prote
14	160.5	8.3	304	B83541	probable polynucle
15	148	7.6	310	S40808	polynucleotide ade
16	147	7.6	310	A91227	probable endonucle
17	148	7.6	310	G86073	probable endonucle
18	131.5	6.8	295	B93597	probable polynucle
19	129	6.7	302	A10950	probable acyltrans
20	127	6.6	294	D82371	probable polynucle
21	124.5	6.4	391	T15366	hypothetical prote
22	121	6.3	303	A48600	probable sm2-acyl9
23	120	6.2	225	B45582	probable 1-acygly
24	120	6.2	245	S20460	1-acylglycerol-3-p
25	120	6.2	245	A80888	1-acyl-glycerol-3-
26	119	6.1	279	T50125	probable 1-acygly
27	117.5	6.1	281	S60477	1-acylglycerol-3-p
28	115.5	6.0	240	D64089	1-acylglycerol-3-p
29	115.5	6.0	363	T20608	hypothetical prote

SUMMARIES

S52645
 Probable 1-acyl-glycerol-3-phosphate acyltransferase - maize
 C:Species: Zea mays (maize)
 C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19-May-2000
 C:Accession: S52645
 R:Brown, A.P.; Coleman, J.; Tomney, A.M.; Watson, M.D.; Slabas, A.R.
 Plant Mol. Biol. 26, 211-223, 1994
 A:Title: Isolation and characterisation of a maize cDNA that complements a 1-acyl sn-gly-her acyltransferase.
 A:Reference number: S52645; MUID:95035993; PMID:7948871
 A:Accession: S52645
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-374 <BRO>
 A:Cross-references: EMBL:Z29518; NID:9575959; PIDN:CAA82638.1; PID:9575960
 C:Superfamily: probable membrane protein YBR042c

Query Match 75.0%; Score 1450.5; DB 2; Length 374;
 Best Local Similarity 70.7%; Pred. No. 1.4e-118;
 Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MATAAAAVVPVPLGLLFFASGLLVNLQAIQCYVVRPVSKSLYRINRVVAELLWLELWVL 60
 DB 1 MAIPLVVLPVPLGLLFLSLGLLVNIAQVLFVIRPFSKSYRINRVLAELLWLVVW 60
 QY 61 IDWAGVKVQIFDTHETFRMLMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 120
 DB 61 VDWAGVKVQVLADEEYRSMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 120
 QY 121 SSKFLPVIGSMFSEYLFERSWAKDESTLKSIGIQRSLSDPFLPFWLALFVEGTRFTQAK 180
 DB 121 SSKFLPVIGSMFSEYLFERSWAKDESTLKSIGIQRSLSDPFLPFWLALFVEGTRFTQAK 180
 QY 181 LLAQEVATSTGLPVRNVLIPRTKGFVSAVSHRSPVPAIYDVTVVAIPKSSPAPTMRL 240
 DB 181 LLAQEVAAQGLPAPRNVLIPRTKGFVSAVSHRSPVPAIYDVTVVIVPKDSQPPTMLRI 240
 QY 241 FKQSPVSVVHHKRLMKELPDTDEAVQACRDI FVAKDALLDKHMAEGTFSQDELQDTG 300
 DB 241 LKQSSVIVHVRMKRHAMSEPKSDEVDKWKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
 QY 301 RPKSLVIVSWACLVVAGSVKFLQSSLLSSKMGVAFSAFGLAVVTALMQILIQFSQSE 360
 DB 300 RPKSLVIVSWACLVVAGSVKFLQSSLLSSKMGVAFSAFGLAVVTALMQILIQFSQSE 359
 QY 361 RSNPAKIVPAKSNK 375
 DB 360 RSSSARAARNRVKKE 374

RESULT 3
 D96550
 Hypothetical protein Film15.12 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 01-Mar-2002
 C:Accession: D96550
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: D96550
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-376 <STO>

A:Gene: Film15.12
 A:Map position: 1
 C:Superfamily: probable membrane protein YBR042c

Query Match 66.0%; Score 1277; DB 2; Length 376;
 Best Local Similarity 62.3%; Pred. No. 1.8e-103;
 Matches 228; Conservative 62; Mismatches 76; Indels 0; Gaps 0;

QY 1 MAIAAAVVPVPLGLLFFASGLLVNLQAIQCYVVRPVSKSLYRINRVVAELLWLELWVL 60
 DB 1 MKIPAAVLPVPLGLLFLSLGLLVNIIQVFFIIVRPSRSLYRINKNVALLWLIWL 60
 QY 61 IDWAGVKVQIFDTHETFRMLMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 120
 DB 61 FDMWACIKINLYDAETLELIGKEHALVISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 120
 QY 121 SSKFLPVIGSMFSEYLFERSWAKDESTLKSIGIQRSLSDPFLPFWLALFVEGTRFTQAK 180
 DB 121 EAKYLPVIGSMFSEYLFERSWAKDESTLKSIGIQRSLSDPFLPFWLALFVEGTRFTQAK 180
 QY 181 LLAQEVATSTGLPVRNVLIPRTKGFVSAVSHRSPVPAIYDVTVVAIPKSSPAPTMRL 240
 DB 181 LEAAQEVASIRSLSPRNVLIPRTKGFVSAVSEIRSPVPAIYDCTLVHNNQPTFTLRL 240
 QY 241 FKQSPVSVVHHKRLMKELPDTDEAVQACRDI FVAKDALLDKHMAEGTFSQDELQDTG 300
 DB 241 FSGOSSEINLQMRHKKSELPETDDGIAQWCQDLFITKDAQLEKYFTKQVFSLEVHQIN 300
 QY 301 RPKSLVIVSWACLVVAGSVKFLQSSLLSSKMGVAFSAFGLAVVTALMQILIQFSQSE 360
 DB 301 RPKPLVIVSWACLVVAGSVKFLQSSLLSSKMGVAFSAFGLAVVTALMQILIQFSQSE 360
 QY 361 RSNPAK 366
 DB 361 RSTPAK 366

RESULT 4
 T06755
 Probable glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) - Arabidopsis thaliana
 A:Alternate names: protein F15B8.160
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-May-2000
 C:Accession: T06755
 R:Quetier, F.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Salanoubat, M.; Mewes, submitted to the Protein Sequence Database, April 1999
 A:Reference number: 215794
 A:Accession: T06755
 A:Molecule type: DNA
 A:Residues: 1-310 <QUE>
 A:Cross-references: EMBL:AL049660; GSPDB:GN00061; ATSP:F15B8.160
 A:Experimental source: cultivar Columbia; BAC clone F15B8
 C:Genetics:
 A:Gene: ATSP:F15B8.160
 A:Map position: 3
 A:Introns: 26/3; 46/3; 72/3; 125/3; 167/3; 198/3; 227/3
 C:Superfamily: probable membrane protein YBR042c
 C:Keywords: acyltransferase; coenzyme A

Query Match 60.0%; Score 1161.5; DB 2; Length 310;
 Best Local Similarity 61.3%; Pred. No. 1.6e-93;
 Matches 228; Conservative 30; Mismatches 35; Indels 79; Gaps 1;

QY 3 IAIAAAVVPVPLGLLFFASGLLVNLQAIQCYVVRPVSKSLYRINRVVAELLWLELWVL 62
 DB 2 VIAAAVLPVPLGLLFFISGLAVNLF----- 25
 QY 63 WWAGVKVQIFDTHETFRMLMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 122
 DB 26 -----QRSGLGSALAVMKKS 42

Db 43 KFLPVIGNSWMTSEYFLERNWAKDESTLKSGLQRLSDPFRPFWLALFVEGTRFTTEAKLK 102

QY 183 AAQYATSTGLPVRNVLIPTRTKGFVS AVSHMRSFVPALYDVTVVAIPKSSPAPTMLRPFK 242

Db 103 AAQYAAASSELPIPRNVLIPTRTKGFVS AVSNMRSFVPALYDVTVVAIPKSSPAPTMLRPFK 162

QY 243 QPSVHVHVKHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGFSDQELQDTGRP 302

Db 163 QPSVHVHVKHSMKDLPESDDAIAQWCRDQFVAKDALLDKHIAADTPPGQEQONIGRP 222

QY 303 IKSLVVISWACLVVAGSVKFLQWSLLSSWKGVAFAFGLAVVTLMAQILIQFSQSERS 362

Db 223 IKSLAVVSWACVLTIGAKFLHWAOLFSSWKGITITISALGLGIITLCMQILIRSSQSERS 282

QY 363 NPAKIVPAKSKN 374

Db 283 TPAKVVPAPKPD 294

RESULT 5

T07936

probable glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) - rape

N;Alternate names: 1-acyl-sn-glycerol-3-phosphate acyltransferase

C;Species: Brassica napus (rape)

C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 20-Jun-2000

C;Accession: T07936

R;Brough, C.L.J.

submitted to the EMBL Data Library, June 1995

A;Reference number: Z16230

A;Accession: T07936

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-311 <EO>

A;Cross-references: EMBL:Z49860; NID:g1149594; PIDN:CAA90019.1

A;Experimental source: cv. jet neuf; embryo

C;Superfamily: probable membrane protein YBR042c

C;Keywords: acyltransferase; coenzyme A

Query Match 59.8%; Score 1156.5; DB 2; Length 311;

Best Local Similarity 61.4%; Pred. No. 4.5e-93;

Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;

QY 5 AAAYVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWELVLDWM 64

Db 4 AAAYVPLGLLFFTSGLVGNLL----- 25

QY 65 AGVKVQIFTDHETFRMLGKEHALVISNHRSDIDLVGWVSAQSGCLGSTFLAVMKSSKF 124

Db 26 -----QRSGCLGSALAVMKSSKF 44

QY 125 LPVIGSMWTFSEYFLERSWAKDESTLKSGLQRLSDPFRPFWLALFVEGTRFTQAKLLAA 184

Db 45 LPVIGSMWTFSEYFLERNWAKDESTLKSGLQRLNDPFRPFWLALFVEGTRFTTEAKLXAA 104

QY 185 QYATSTGLPVRNVLIPTRTKGFVS AVSHMRSFVPALYDVTVVAIPKSSPAPTMLRPFKQ 244

Db 105 QYAAASSELPIPRNVLIPTRTKGFVS AVSNMRSFVPALYDVTVVAIPKSSPAPTMLRPFKQ 164

QY 245 PSVVHVHVKHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGFSDQELQDTGRPIK 304

Db 165 PSVVHVHVKHSMKDLPESEDAIAQWCRDQFVTKDALLDKHIAADTFAGQKEQNGRPIK 224

QY 305 SLLVVISWACLVVAGSVKFLQWSLLSSWKGVAFAFGLAVVTLMAQILIQFSQSERSNP 364

Db 225 SLAVVLSWACILITIGAKFLHWSNLFSSWKGIALSALGLGIITLCMQILIRSSQSERS 284

QY 365 AKIVPAKSKN 374

Db 285 AKVAPAKPKD 294

RESULT 6

B96780

hypothetical protein P9E10.13 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: B96780

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 815-820, 2000

A;Authors: Hunter, J.B.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Matti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salberg, S.L.; Scherwitz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: B96780

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-393 <STO>

A;Cross-references: GB:AB005173; NID:G6646762; PIDN:AAF21074.1; GSPDB:GN00141

C;Genetics:

A;Gene: P9E10.13

A;Map position: 1

Query Match 21.4%; Score 414; DB 2; Length 393;

Best Local Similarity 34.2%; Pred. No. 3.1e-28;

Matches 106; Conservative 52; Mismatches 132; Indels 20; Gaps 6;

QY 9 VVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRI-----NRVWAE-----LWLEL-VW 59

Db 17 LTPULIRGLMLLVFUSTAFMFLYFAPIALGLRLSSVQQRKRVSLIFGLWMLWPY 76

QY 60 LIDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDLVGWVSAQSGCLGSTLAVMK 119

Db 77 LFETVNGTIVFSGD-----IIPVEKRVLLIANHRTVEDVMYLNIALRKGCGLGVIKYVLK 132

QY 120 KSSKFLPVIGSMWTFSEYFLERSWAKDESTLKSGLQRLSDPFRPFWLALFVEGTRFTQAA 179

Db 133 SSLMKLPIFGMFGPHVLEFIPVERKREVDPEVLLQWLSFKDQPSFLWALPEGDFTEE 192

QY 180 KLLAAQYATSTGLPVRNVLIPTRTKGFVS AVSHMRSFVPALYDVTVVAIPKSSPAPTMLR 239

Db 193 KCRSQKFAAEVGLPALSNNLLPKTRGFCVCLVHLNSLDVAYDLTIAYKRCPS-FWDN 251

QY 240 LFKGQPSVVHVHVKHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGFSDQELQDT 299

Db 252 VEGTDPSEVHIHVRVLLKEIPANEAESSAWLMDSFKLKDKLLSDFNAGKFPNQ----- 306

QY 300 GRPIKSILVV 309

Db 307 -RPEBELSVL 315

RESULT 7

T40466

probable acetyltransferase protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 01-Mar-2002

C;Accession: T40466

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.

submitted to the EMBL Data Library, November 1998

A;Reference number: Z21931

A;Accession: T40466

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-350 <LYN>

A;Cross-references: EMBL:AL034382; PIDN:CAA22289.1; GSPDB:GN00067; SPDB:SPBC428.14

A;Experimental source: strain 972h-; cosmid c428

C;Genetics:

A;Gene: SPDB:SPBC428.14

A;Map position: 2

C;Superfamily: probable membrane protein YBR042c

Query Match 16.0%; Score 310.5; DB 2; Length 350;
Best Local Similarity 27.1%; Pred. No. 2.8e-19;
Matches 84; Conservative 62; Mismatches 133; Indels 31; Gaps 8;
QY 37 VSKSLYR---INRVVALLWLELVLDWAGVVKVQIFDTHETFR-----MG 82
DB 36 VNKELYNKYIAFTKSFAGILFTALVQL---FSPTPTVLTVDPELNLFYLDNRGCLLETTA 92
QY 83 KEHALVTSNHSRSDIDWLVGVSAQSCGLSTLAVMKSKKFLPVIGWMMFSEYLFLE 142
DB 93 AERNIVIANHQLYSDMWVYVWMLSTAKQGHVIMLKNSLKWLPVIGWQOLFPRIFLGR 152
QY 143 SWAKDESTLXSGIQRLSDFFLPFWLALFVEGTFRTOAKLLAAOEYATSTGLPVRNVLIP 202
DB 153 KWDKDYETMSGRHFKFIRNVRDSVSLIFPEGTNLVESTYQSRVYADKIGVKMPKHLMLP 212
QY 203 RTKGFVSAVSHMRSFVPAIYDVTVVAIPKSSP-----APTMRL-LFKGP-SVVHVHIXR 254
DB 213 RVRLGFSISQLRDSMTLYDYTFYFSDPKPKYAADAFSLPKLFFEGVPIKELHIXVR 272
QY 255 HLMKELPDTEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTGRPIKSLLVVIS--- 311
DB 273 FPISIEITFEEDQFTDWLYQRYWEKDKLIDTLLTGTGNFPGPKLHTTVRLKGRLEILSLFS 332
QY 312 --WACLIVVAG 319
DB 333 VLFTC-IVAG 341
RESULT 8
T31913
hypothetical protein T05H4.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C/Accession: T31913
R/Blanchard, M.
submitted to the EMBL Data Library, July 1997
A/Description: The sequence of C. elegans cosmid T05H4.
A/Reference number: Z21097
A/Accession: T31913
A/Status: preliminary; translated from GB/EMBL/DDJ
A/Molecule type: DNA
A/Residues: 1-344 <BLA>
A/Cross-references: EMBL:AF016452; PIDN:AA866008.1; GSPDB:GN00023; CBSP:T05H4.1
A/Experimental source: strain Bristol N2; clone T05H4
C/Genetics:
A/Gene: CBSP:T05H4.1
A/Map position: 5
A/Introns: 55/3; 212/1; 243/3; 298/3

Query Match 14.8%; Score 287; DB 2; Length 344;
Best Local Similarity 26.7%; Pred. No. 3e-17;
Matches 92; Conservative 64; Mismatches 157; Indels 32; Gaps 12;
QY 14 LFFASGLLVNLIQAICYVVRVPSKSLYR-INRVVALLWLELVLDWAGVVKVQI 71
DB 11 VLVFSSLLGTVELLPFLIPLAWFAFKLWRTCADRLVG--FWLTTPCSLIEWFGV--- 64
QY 72 FTDHETFLMG-----KEHALVTSNHSRSDIDWLVGVSAQSCG--CLGSTLAMKSKK 124
DB 65 ----NFRVTGDIIEDEFAILIMHRTDLDFWLSNALYKMDPWLTLTETSLKAPLKK 119
QY 125 LPVIGSMFMFSEYLFLEERSWAKDESTLXSGIQRLSDFFLPFWLALFVEGTFRTOAKLLAA 184
DB 120 IPGAGWMSGGSYIFLDNFENDKPVLEIRIVKYSGSEKKYQILFAEGTDKGEATRLS 179
QY 185 QEYATSTGLPVRNVLIPRTKGFVSAVSHMR--SFVPAIYDVTVVAIPKSSPAPTMLRFLK 242
DB 180 DAFADKNGLPRVEYVJLHPTTGFKFLMELMKENVIKYYVDLTIAV-SGTIVDTDEAKLLA 238
QY 243 GO-PSVVHVHIXRMLKELPDTEAVAQWCRDIFVAKDALLDK-----HMAEGTFSDOEL 296

QY 297 QDTGRPIKSLLVVISW--ACLIVAGSVKFLQWSSLLSSWKGVAFS 339
DB 298 PETTIGIYVAFAPFWLASLIWNGAIYSLLMVKVINRFRYGCYS 342
RESULT 9
S45900
Probable membrane protein YBR042c - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YBR042c
C/Species: Saccharomyces cerevisiae
C/Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
C/Accession: S45900
R/Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.
submitted to the Protein Sequence Database, August 1994
A/Reference number: S45893
A/Accession: S45900
A/Molecule type: DNA
A/Residues: 1-397 <AND>
A/Cross-references: EMBL:Z35911; NID:G536265; PIDN:CAA84984.1; PID:G536266; GSPDB:GN00000
A/Experimental source: strain S288C
C/Genetics:
A/Gene: MIPS:YBR042c
A/Cross-references: SGD:S0000246
A/Map position: 2R
C/Superfamily: probable membrane protein YBR042c
C/Keywords: transmembrane protein
F:12-37/Domain: transmembrane #status predicted <TM1>
F:55-77/Domain: transmembrane #status predicted <TM2>
F:134-150/Domain: transmembrane #status predicted <TM3>
F:372-390/Domain: transmembrane #status predicted <TM4>

Query Match 14.0%; Score 271; DB 2; Length 397;
Best Local Similarity 24.6%; Pred. No. 9.2e-16;
Matches 87; Conservative 72; Mismatches 122; Indels 72; Gaps 13;
QY 8 VVWP-LGILLFPASGLLVNLIQAICYVVRVPSKSLY-----RRINRVVALLWLELV-W 59
DB 13 VVVEGSLILFFQGCILLFLQLTY-----KTLYCRNDIRKQIGLNTKRLFIVLVS 65
QY 60 LIDWAGVVKVQIFTDHE-----TF-----RLMG--KEHALVTSNHSRSDIDWLVGVSA 105
DB 66 ILHVVASAVRITITENSVPKGTFFLDLKKRILSHLKSNSVAICNHQIYTDHIFLWLA 125
QY 106 QRSCLGSTLAVMKSKKFLPVIGWMMFSEYLFLEERSWAKDESTLXSGI----- 155
DB 126 YTSNLGANFIIILKKSLASIPILGFGMRNYNFIFMSRKWAQDKITLSNLSLADSNARGA 185
QY 156 -----QRLSD-----FPLPFWLALFVEGTFRTOAKLLAAOEYATSTG 192
DB 186 GSLACKSPERITSEGESIWNPEVIDPKQIHWPVNLILFPEGTNLSDATROKSKYAAKIG 245
QY 193 LPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVVAIP--KSSPAPTMLRFLK-----Q 244
DB 246 KKPEKNVLLPHSTGLRYSLOKLKPSIESLYDITIGYGVKQEBYBELIYGLKXIFLEGKY 305
QY 245 PSVVHVHIXRMLKELPDTE-VAQWCRDIFVAKDALLDKHMAEGTF-SDQE 295
DB 306 PKLVDIHIRAFDVKDIPLEDENEFSEWLYKINSEKDALMERYYSTGFSVSDPE 358

RESULT 10
T34057
hypothetical protein F28B3.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C/Accession: T34057
R/Gaisel, C.; Kramer, J.; Smith, A.
submitted to the EMBL Data Library, May 1997
A/Description: The sequence of C. elegans cosmid F28B3.
A/Reference number: Z21469
C/Genetics: T34057

Query Match	13.9%;	Score	269;	DB	2;	Length	918;		
Best Local Similarity	26.3%;	Pred. No.	4.2e-15;						
Matches	88;	Conservative	67;	Mismatches	119;	Indels	60;	Gaps	11;
QY	1	MAIAAAVVVPLGLLF	----	FASGLLVNLIQAICVWVRPSKSI	-----	YRINRV	48		
DB	539	IADVLRPIPCSLLSLWVFPASCAIV	--	IGVSWIVPRHVAQQDNNMFKYSYMRCLCF			596		
QY	49	VAELLWLELVMLIDWAGVKVQF	-	TDHETFRLMGK-EHALVTSNHRSDIDMLWGVWSAQ			106		
DB	597	VFENL	-----	SGVEIYLHGINEEVVWKTGPENAVMISSHQSNVDWIIPVMLAA			645		
QY	107	RSCCLGSTA	--	VMKSSKFLPVIGSWMFSYFLFLERSWAKDESTLKSIGIORLSDFFPL			163		
DB	646	RHGQGNQAFRYVMVXNSIHLVFMFGYIIPQHGYIVYRREGF	IGAPVLFQQLKWLNSDP				705		
QY	164	PFWLALFVSGTRFTQAK	--	LLAAQEVATSTGLVPVRNVLI	PRTKGFSVASVHMRSPVA		230		
DB	706	PYMLLIPPEGTRNSAKKHILLSSNRFLKSGRQPMQNVLCPSGGQLQALDNL	-	STLDA			764		
QY	221	IYDVTV	-----	AIPKSPAPTMLRFLFKG	-----	QPSVVVHHIKR	254		
DB	765	IYDVTVMYQMRFDLGLNLT	IIHYNLLIIYMAERGLAPGMFPCCGSQFQQLHIHLDR				824		
QY	255	HLMKELPDDTDEAVAQWCRDIFVAKDALLDKHMAE					288		
DB	825	IPIDEVPKAKLELRTWTIERFTTKERLIDBFYSE					858		

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Query Match      12.9%; Score 250; DB 2; Length 439;
Best Local Similarity   25.1%; Pred.No. 7.1e-14;
Matches        65; Conservative S4; Mismatches 106; Indels   34; Gaps    4;

Qy      60 LIDWAGCVKQIFDHEFERLMGKEHALVSNHESDIDLWGVSQAORSG--CLGSTLAV 117
          |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      21 LLBFLMGVRIRVSGDETEF---GSPANIYNNHRTLRDWMIMWCALCIINPWLITSNKIS 76

Qy     118 MKSSKFLPVIGSMWFSEYLFLERSWAKDESTLKSGIQRLSDPFLPFWALFVEGRFT 177
          ||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db     77 LKAQLKLLPGAGFGMAAAQGVFLERNAEVDKRSFDADLYFKNIDKKYQILLFPFGTDKS 136

Qy     178 QAKLLAAQEYATSTGLVPVRNVLLIPRTKGFFVSVAVSHMR----- 215

Db    137 EWTTLKREFAKNGLRHLDDVLYPRITGTGFIHLNKVREPSSSVIRFNKVHFYFIKIQQ 196
```

Query Match	12.8%;	Score	247;	DB	2;	Length	396;
Best Local Similarity	25.6%;	Pred.	No. 1.le-13;				
Matches	85;	Conservative	61;	Mismatches	12;	Indels	54; Gaps 11;
Qy	17	FASGLLVNIQIAICVYVRPVSKSYRR-INRVVAELLWLELVLWLIDNWAGVKVQIFTDH	75				
Dd	33	FTSGLSIYVFQICQLVLPWSKIRFQINGIKKAFTVL-LCMTLNVAPSSLNV--TF	89				
Qy	76	EYFRLLMG-----KEHALVTISNHRSDIDNLVGVSQAQRSCGLSTTAVMKKSFK	124				
Dd	90	ETSRPLKNSNAKPCFPKDRDRAIIITANCOMYADVIIKLWLSFVSLNGGVNVIILKKALQY	149				

Qy	125	LPVIGSMWPFSSYLFILERSWAKDSTL-----KGIOQLSDPPLP	164
Dd	150	IPLLFGFMENFFKFI FLSLRNWKQEKALNTSLSVMSDLNARCKGPLTNKYSCYSKTNESTAA	209
Qy	165	FWLALFVEGTRE---TQAKLLAAQEYATSTCLPYPRNVLIPTRKGFVSVAWSHRSPVPAI	221
Dd	210	YNLIIMPPEGTNUSLTREKSAPCORAHLDHVQL-RHLLPHSGKLKFAVEKIAPLSLDAI	268
Qy	222	YDVTVAI PKSSPAP-----TWLRLF--KGOPSVVVHHIKRHLMKELP-DTDEAVAQ	269
Dd	269	YDVTICY---SPALSTEYVGTFKLIKFLMGVYYPEKVDFYIREFRVNIPIQQDDEVFN	325
Qy	270	WCERDFVAKDLLDKHMAEGTFSQDELQD	298
Dd	326	WLLGVYWEKDQLLEDYYNTGTFKSNAKND	354

RESULT 13

T25998

hypothetical protein ZK40.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T25998

R:Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid ZK40.

A:Reference number: Z20121

A:Accession: T25998

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-533 -BRA>

A:Cross-references: EMBL:U64839; PIDN:AAB04844.1; GSPDB:GN00023; CESP:ZK40.1

A:Experimental source: strain Bristol N2; clone ZK40

C:Genetics:

A:Gene: CESP:ZK40.1

A:Map position: 5

A:Introns: 7/1: 38/3; 126/3; 93/3; 160/1; 301/3; 422/2; 472/3

RESULT 14
B83541
probable polynucleotide adenylyltransferase (EC 2.7.7.19) II PA0834 [similarity] - Pseud
C.Species: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Mar-2001
C.Accession: B83541

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: AB2950; MUID:20437337; PMID:10984043

A;Accession: B83541

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-304 <STO>

A;Cross-references: GB:AE004518; GB:AE004091; NID:g9946725; PIDN:AAG04223.1; GSPDB:GNC001

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA0834

C;Superfamily: Escherichia coli polynucleotide adenyllyltransferase II yibG

C;Keywords: nucleotidyltransferase

RESULT 15
S40808
polynucleotide adenyllyltransferase (EC 2.7.7.19) II yihg [validated] - Escherichia coli
C:Species: Escherichia coli
C:Date: 19-May-1994 #sequence_revision 01-Sep-1995 #text_change 01-Mar-2002
C:Accession: S40808; J06149; B65191
R:Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 21, 3391-3398, 1993
A:title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from 8
A:Reference number: S40802; MUID:93347969; PMID:8346018
A:Accession: S40808
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-310 <PLU>
A:Cross-references: EMBL:L19201; NID:G304961; PIDN:AAB02997.1; PID:G304968
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
R:Cao, G.J.; Pogliano, J.; Sarkar, N.
Proc. Natl. Acad. Sci. U.S.A. 93, 11580-11585, 1996
A:title: Identification of the coding region for a second poly(A) polymerase in Escherichia coli
A:Reference number: J06149; MUID:97030237; PMID:8876178
A:Accession: J06149
A:Molecule type: DNA
A:Residues: 1-310 <CAO>
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:title: The complete genome sequence of Escherichia coli K-12

Search completed: July 7, 2004, 13:41:49
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2004, 13:41:23 ; Search time 51 Seconds

(without alignments)
2301.059 Million cell updates/sec

Title: US-09-914-098-56

Perfect score: 1935

Sequence: 1 MAIAAAAVVPLGLFPASG.....QSRSPAKIVPAKSNKGS 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1935	100.0	377	12	US-10-424-599-278313
2	1771	91.5	342	12	US-10-425-114-47952
3	1765.5	91.2	419	12	US-10-424-599-210085
4	1731	89.5	406	12	US-10-425-114-57801
5	1695	87.6	399	12	US-10-425-114-51954
6	1592	82.3	319	12	US-10-424-599-278291
7	1523	78.7	377	8	US-08-818-581B-4
8	1459.5	75.4	425	12	US-10-425-114-67316
9	1451.5	75.0	419	12	US-10-425-114-66105
10	1450.5	75.0	374	9	US-09-970-989-5
11	1450.5	75.0	374	12	US-10-667-494-5
12	1450.5	75.0	374	16	US-10-667-462-5
13	1450.5	75.0	374	16	US-10-667-464-5
14	1442.5	74.5	375	8	US-08-818-581B-5
15	1438.5	74.3	374	16	US-10-437-963-130474

16	1301	67.2	380	12	US-10-425-114-49811	Sequence 49811, A
17	1156.5	59.8	311	8	US-08-818-581B-6	Sequence 6, Appli
18	999.5	51.7	263	12	US-10-425-114-70268	Sequence 70268, A
19	899.5	46.5	233	12	US-10-425-114-51896	Sequence 51896, A
20	856	44.2	266	12	US-10-425-114-58564	Sequence 58564, A
21	628	32.5	368	10	US-09-946-374-297	Sequence 297, App
22	628	32.5	368	12	US-10-206-915-338	Sequence 338, App
23	628	32.5	368	12	US-10-199-670-338	Sequence 338, App
24	628	32.5	368	12	US-10-201-858-338	Sequence 338, App
25	628	32.5	368	12	US-10-205-890-338	Sequence 338, App
26	628	32.5	368	12	US-10-208-024-338	Sequence 338, App
27	628	32.5	368	12	US-10-174-581-338	Sequence 338, App
28	628	32.5	368	12	US-10-176-483-338	Sequence 338, App
29	628	32.5	368	12	US-10-176-749-338	Sequence 338, App
30	628	32.5	368	12	US-10-176-914-338	Sequence 338, App
31	628	32.5	368	12	US-10-176-915-338	Sequence 338, App
32	628	32.5	368	12	US-10-1006-485A-297	Sequence 297, App
33	628	32.5	368	12	US-10-013-907A-297	Sequence 297, App
34	628	32.5	368	12	US-10-015-499A-297	Sequence 297, App
35	628	32.5	368	12	US-10-176-484-338	Sequence 338, App
36	628	32.5	368	12	US-10-180-550-338	Sequence 338, App
37	628	32.5	368	12	US-10-183-014-338	Sequence 338, App
38	628	32.5	368	12	US-10-187-738-338	Sequence 338, App
39	628	32.5	368	12	US-10-187-740-338	Sequence 338, App
40	628	32.5	368	12	US-10-187-883-338	Sequence 338, App
41	628	32.5	368	12	US-10-194-363-338	Sequence 338, App
42	628	32.5	368	12	US-10-194-460-338	Sequence 338, App
43	628	32.5	368	12	US-10-194-463-338	Sequence 338, App
44	628	32.5	368	12	US-10-194-484-338	Sequence 338, App
45	628	32.5	368	12	US-10-194-484-338	Sequence 338, App

ALIGNMENTS

RESULT 1

US-10-424-599-278313

Sequence 278313, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424.599

CURRENT FILING DATE: 2003-04-28

NUMBER-OF-SEQ ID NOS: 285684

SEQ ID NO 278313

LENGTH: 377

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_9333C.1.pep

US-10-424-599-278313

Query Match	100.0%	Score	1935	DB	12	Length	377
Best Local Similarity	100.0%	Pred. No.	8.4e-195	Mismatches	0	Indels	0
Matches	377	Conservative	0	Gaps	0		
QY	1	MAIAAAVVPGLGLFPASGLVNLIOAICVYVVRPVSKSLYRINRVVAELWLEVL	60				
Db	1	MAIAAAVVPGLGLFPASGLVNLIOAICVYVVRPVSKSLYRINRVVAELWLEVL	60				
QY	61	IDWAGVKVQIETDHEFRMLGKEHALVISNHSDDTLVGWVSAGRSGLSTLAVMKK	120				
Db	61	IDWAGVKVQIETDHEFRMLGKEHALVISNHSDDTLVGWVSAGRSGLSTLAVMKK	120				
QY	121	SSKLPVIGSMWFSEYLFPLERSWAKDESTKSGIORLSDFPLFPFWLAFVEGTRFTQAK	180				
Db	121	SSKLPVIGSMWFSEYLFPLERSWAKDESTKSGIORLSDFPLFPFWLAFVEGTRFTQAK	180				

QY 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASHMRSFVPAIYDVTVVAIPKSSPAPTMRL 240
Db 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASHMRSFVPAIYDVTVVAIPKSSPAPTMRL 240
QY 241 FKQPSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTG 300
Db 241 FKQPSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTG 300
QY 301 RPKSLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360
Db 301 RPKSLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360
QY 361 RSNPAKIVPAKSKNKS 377
Db 361 RSNPAKIVPAKSKNKS 377
RESULT 2
US-10-425-114-47952
; Sequence 47952, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47952
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700909008_FLI.pap
US-10-425-114-47952

Query Match 91.5%; Score 1771; DB 12; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.4e-177;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 PVSKSLYRINRVVAELWLELWLDWAGVKQIETDHTFRLMGKEHALVISNHRSD 95
Db 1 PVSKSLYRINRVVAELWLELWLDWAGVKQIETDHTFRLMGKEHALVISNHRSD 60
QY 96 IDWLGVWVSAQSGCLGTLAVMKSSKFLPVIGNSWMPSEYLFPLERSWAKDESLKSGI 155
Db 61 IDWLGVWVSAQSGCLGTLAVMKSSKFLPVIGNSWMPSEYLFPLERSWAKDESLKSGI 120
QY 156 QRLSDFFLPFWLAFVEGTRFQAKLLAAQAEYATSTGLPVRNVLIPRTKGFVSASHMR 215
Db 121 QRLSDFFLPFWLAFVEGTRFQAKLLAAQAEYATSTGLPVRNVLIPRTKGFVSASHMR 180
QY 216 SFVPAIYDVTVVAIPKSSPAPTMRLFKQPSVHVHVKRHLMKELPDTDEAVAQWCRDIF 275
Db 181 SFVPAIYDVTVVAIPKSSPAPTMRLFKQPSVHVHVKRHLMKELPDTDEAVAQWCRDIF 240
QY 276 VAKDALLDKHMAEGTFSQDELQDTGRPIKSLVVISWACLWVAGSVKFLQWSSLLSSWKG 335
Db 241 VAKDALLDKHMAEGTFSQDELQDTGRPIKSLVVISWACLWVAGSVKFLQWSSLLSSWKG 300
QY 336 VAFSAFGLAVVTALMQILIQFSQSERNSNPAKIVPAKSKNKS 377
Db 301 VAFSAFGLAVVTALMQILIQFSQSERNSNPAKIVPAKSKNKS 342

RESULT 3

US-10-424-599-210085
; Sequence 210085, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210085
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31735C.1.pap
US-10-424-599-210085
Query Match 91.2%; Score 1765.5; DB 12; Length 419;
Best Local Similarity 91.9%; Pred. No. 7.1e-177;
Matches 340; Conservative 12; Mismatches 17; Indels 1; Gaps 1;
QY 6 AAVVPLGLLFFASGLLVNLIQAIQVYVVRPVSKSLYRINRVVAELWLELWLDWMA 65
Db 38 SAVVPLGLLFFASGLLVNLIQAIQVYVVRPVSKSLYRINRVVAELWLELWLDWMA 97
QY 66 GVKQIETDHTFRLMGKEHALVISNHRSDIDWLGVWVSAQSGCLGTLAVMKSSKFL 125
Db 98 GVKQVETDHTFRLMGKEHALVISNHRSDIDWLGVWVSAQSGCLGTLAVMKSSKFL 157
QY 126 PVIGNSWMPSEYLFPLERSWAKDESLKSGIQLSDPFLPFWLAFVEGTRFQAKLLAAQ 185
Db 158 PVIGNSWMPSEYLFPLERSWAKDESLKSGIQLSDPFLPFWLAFVEGTRFQAKLLAAQ 217
QY 186 EYATSTGLPVRNVLIPRTKGFVSASHMRSFVPAIYDVTVVAIPKSSPAPTMRLFKQOP 245
Db 218 EYAAAGLPVRNVLIPRTKGFVSASHMRSFVPAIYDVTVVAIPKSSPAPTMRLFKQOP 277
QY 246 SVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTGRPIKS 305
Db 278 SVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTGRPIKS 337
QY 306 LLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSERNSPA 365
Db 338 LLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSERSTPS 397
QY 366 KIVPA-KSKN 374
Db 398 KIVPA-KSKN 407

RESULT 4
US-10-425-114-57801
; Sequence 57801, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57801

LENGTH: 406
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701127504_FLI.pap
US-10-425-114-57801

Query Match 89.5%; Score 1731; DB 12; Length 406;
Best Local Similarity 89.4%; Pred. No. 2.9e-173;
Matches 330; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

QY 6 AAVVPLGLFFASGLLVNLQICVYVVRPVSKSLYRNRINRVVAELLWLELWIDWA 65
DB 26 AVVVPLGLFFASGLLVNLQICVYVVRPVSKSLYRNRINRVVAELLWLELWIDWA 85

QY 66 GVKVQIFDTHETFRMGKHEALVISNHRSDIDWLVGWSAORSGLGSLTAVNKKSKFL 125
DB 86 GVKVQVFTDPTFRSGKHEALVISNHRSDIDWLVGWSAORSGLGSLTAVNKKSKFL 145

QY 126 PVIGSMWFSEYLFRLSKWAKDESTLKSGIQRLSDPFLPFWLALFVEGTRFTQAKLLAAQ 185
DB 146 PVIGSMWFSEYLFRLSKWAKDESTLKSGIQRLSDPFLPFWLALFVEGTRFTQAKLLAAQ 205

QY 186 EYATSTGLPVRNVLIPRTKGFVSANVHMSFVPAIYDVTVAIKSSPAPTMRLFKGOP 245
DB 206 EYAAASAGLPVRNVLIPRTKGFVSANVHMSFVPAIYDVTVAIKSSPAPTMRLFKGRKS 265

QY 246 SVVHVHKKRHKMELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIKS 305
DB 266 SVVHVHKKRHKMELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIKS 325

QY 306 LLVVISWACLVVAGSVKFLQWSLLSSWKGVAFAFGLAVVVTALMQILIOFSOSERSNPA 365
DB 326 LVVVISWACVVVGVVVKFLQWSLLSSWKGVAFAFGLGVVVTLLMHILIMFSQSERSTP 385

QY 366 KIVPAKSKN 374
DB 386 KVAPAKSKN 394

RESULT 5
US-10-425-114-51954
Sequence 51954, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 51954
LENGTH: 399
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700844230_FLI.pap
US-10-425-114-51954

Query Match 87.6%; Score 1695; DB 12; Length 399;
Best Local Similarity 87.8%; Pred. No. 1.8e-169;
Matches 325; Conservative 20; Mismatches 23; Indels 2; Gaps 2;

QY 6 AAVVPLGLFFASGLLVNLQICVYVVRPVSKSLYRNRINRVVAELLWLELWIDWA 65
DB 19 AVVVPLGLFFASGLLVNLQICVYVVRPVSKSLYRNRINRVVAELLWLELWIDWA 78

QY 66 GVKVQIFDTHETFRMGKHEALVISNHRSDIDWLVGWSAORSGLGSLTAVNKKSKFL 125
DB 79 GVKVQVFTDPTFRSGKHEALVISNHRSDIDWL-GWVLAQRSGLGSLTAVNKKSKFL 137

QY 126 PVIGSMWFSEYLFRLSKWAKDESTLKSGIQRLSDPFLPFWLALFVEGTRFTQAKLLAAQ 185
DB 138 PVIGSMWFSEYLFRLSKWAKDESTLKSGIQRLSDPFLPFWLALFVEGTRFTQAKLLAAQ 197

QY 186 EYATSTGLPVRNVLIPRTKGFVSANVHMSFVPAIYDVTVAIKSSPAPTMRLFKGOP 245
DB 198 EYAAASAGLPVRNVLIPRTKGFVSANVHMSFVPAIYDVTVAIKSSPAPTMRLFKGRKS 257

QY 246 SVVHVHKKRHKMELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIKS 305
DB 258 SLVHVHKKRHKMELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTGRPIKS 317

QY 306 LLVVISWACLVVAGSVKFLQWSLLSSWKGVAFAFGLAVVVTALMQILIOFSOSERSNPA 365
DB 318 LVVVISWACVVVGVVVKFLQWSLLSSWKGVAFAFGLGVVVTLLMHILIMFSQSERSTP 377

QY 366 KIVPA-KSKN 374
DB 378 KVAPTKSKN 387

RESULT 6
US-10-424-599-278291
Sequence 278291, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 278291
LENGTH: 319
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(319)
OTHER INFORMATION: unsure at all Xaa locations
OTHER INFORMATION: Clone ID: PAT_MRT3847_9331C.1.pap
US-10-424-599-278291

Query Match 82.3%; Score 1592; DB 12; Length 319;
Best Local Similarity 84.4%; Pred. No. 9.2e-153;
Matches 318; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY 1 MAIAAAVVVPLGLFFASGLLVNLQICVYVVRPVSKSLYRNRINRVVAELLWLELWVL 60
DB 1 MAIAAAVVVPLGLFFASGLLVNLQICVYVVRPVSKSLYRNRINRVVAELLWLELWVL 60

QY 61 IDWAGVKVQIFDTHETFRMGKHEALVISNHRSDIDWLVGWSAORSGLGSLTAVNKK 120
DB 61 IDWAGVKVQIFDTHETFRMGKHEALVISNHRSDIDWLVGWSAORSGLGSLTAVNKK 120

QY 121 SSKFLPVIGSMWFSEYLFRLSKWAKDESTLKSGIQRLSDPFLPFWLALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWFSEYLFRLSKWAKDESTLKSGIQRLSDPFLPFWLALFVEGTRFTQAK 180

QY 181 LLAAGYATSTGLPVRNVLIPRTKGFVSANVHMSFVPAIYDVTVAIKSSPAPTMRL 240
DB 181 LLAAGYATSTGLPVRNVLIPRTKGFVSANVHMSFVPAIYDVTVAIKSSPAPTMRL 240

QY 241 FKQSGSVVHVHKKRHKMELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300

Db 241 FKQPSVVH-----251
QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMOILIQFSQE 360
Db 252 -----IXWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMOILIQFSQE 302
QY 361 RSNPAKIVPAKSKNGS 377
Db 303 RSNPAKIVPAKSKNGS 319

RESULT 7

US-08-818-581B-4
; Sequence 4, Application US/08818581B
; Publication No. US20020007499A1
; GENERAL INFORMATION:
; APPLICANT: SLABAS, Antoni Ryszard
; APPLICANT: BROWN, Adrian Paul
; APPLICANT: BROUGH, Claire Louise
; APPLICANT: KROON, Johannes Theodorus Maria
; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT
; TITLE OF INVENTION: 2-ACYLTRANSFERASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Btentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,581B
; FILING DATE: March 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB96/00306
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: GB 9502468.3
; FILING DATE: 09-FEB-1995
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-818-581B-4

Query Match 78.7%; Score 1523; DB 8; Length 377;
Best Local Similarity 77.3%; Pred. No. 2.2e-151;
Matches 283; Conservative 43; Mismatches 40; Indels 0; Gaps 0;
QY 1 MAIAAAVVVPLGLFFASGLLVNLIQAICYVVPVSKSLYRRINRVVAELLMLELVL 60
Db 1 MAIPAAAFIVPLSLFFNFGSLVNTIQAVFYVYLRPISKDTYRRINTLVAEELMLELVL 60
QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLGVWSAQSGCLGSTLAVMKK 120
Db 61 IDWAGVKVQLYTDHETFRMLGKEHALVICNHRSDIDWLGVLAQRCCGLSSIAVMKK 120
QY 121 SSKFLPVIGWSMWFSEYLFRLMSKAKDESLKSGIQRSLSDPPLPFWALFVEGTRFTQAK 180
Db 121 SSKFLPVIGWSMWFSEYLFRLNWKADENTLKSGLQRLNDFPKPFWALFVEGTRFTKAK 180
QY 181 LLAQGEYATSTGLPVPRNVLIPTKGFVSVAHMSFVPAIYDVTVAIPKSSPAPTMLRL 240
Db 181 LLAQGEYAAAGLPPVPRNVLIPTKGFVSVAHMSFVPAIYDVTVAIPKTPTEQPTMLRL 240
QY 241 FKQPSVVHVKHRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300

Db 241 FKQPSVVHVKHRLMKDLPKTDDGVAQWCKDQFISKDALLDKHVAEDTSGLEVDIG 300
QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMOILIQFSQE 360
Db 301 RPKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMOILIRSSQE 360
QY 361 RSNPAK 366
Db 361 HSTPAK 366

RESULT 8

US-10-425-114-67316
; Sequence 67316, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67316
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4765-008-H3_FLI.pap
US-10-425-114-67316

Query Match 75.4%; Score 1459, 5; DB 12; Length 425;
Best Local Similarity 71.7%; Pred. No. 1.3e-144;
Matches 269; Conservative 48; Mismatches 57; Indels 1; Gaps 1;
QY 1 MAIAAAVVVPLGLFFASGLLVNLIQAICYVVPVSKSLYRRINRVVAELLMLELVL 60
Db 52 MAIPVLVWLPLGLLFLSLVNTIQAILFVIRPFSKSLYRRINRFLAELLMQLVWV 111
QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLGVWSAQSGCLGSTLAVMKK 120
Db 112 VDWAGVKVQLHADEETYSRSGKEHALVISNHRSDIDWLIGWTLAQRSGCLGSTLAVMKK 171
QY 121 SSKFLPVIGWSMWFSEYLFRLMSKAKDESLKSGIQRSLSDPPLPFWALFVEGTRFTQAK 180
Db 172 SSKFLPVIGWSMWFSEYLFRLMSKAKDESLKSGIQRSLSDPPLPFWALFVEGTRFTPAK 231
QY 181 LLAQGEYATSTGLPVPRNVLIPTKGFVSVAHMSFVPAIYDVTVAIPKSSPAPTMLRL 240
Db 232 LLAQGEYAAAGLPPVPRNVLIPTKGFVSVAHMSFVPAIYDVTVAIPKSPQPTMLRI 291
QY 241 FKQPSVVHVKHRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
Db 292 LKQSSVHVVRMGRHMSKSDDDVSKWCKDIFVAKDALLDKHATGTF-DEIRPTG 350
QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMOILIQFSQE 360
Db 351 RPKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMOILIRSSQE 410
QY 361 RSNPAKIVPAKSKNGS 375
Db 411 RSSAKAARNRVKKE 425

RESULT 9

US-10-425-114-66105
; Sequence 66105, Application US/10425114

Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 66105
LENGTH: 419
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4315-045-D3_FLI.pep
US-10-425-114-66105

Query Match 75.0%; Score 1451.5; DB 12; Length 419;
Best Local Similarity 70.9%; Pred. No. 8.7e-144;
Matches 266; Conservative 50; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPGLGILFFASGLLVNLQAICYVVRPVSKSLYRRINRVVAELLWL 60
DB 46 MAIPLVVLVPLGLLFLSGLVNTQAIFVTIRPFKSLYRRINRFLAELLWLQVWV 105
QY 61 IDWAGVKVQIFTDHETFRMGKEHALVISNHRSDIDLVGVWSAQRSGCLSTLAVMKK 120
DB 106 VDWAGVKVQLHADEITYRSMGKEHALVISNHRSDIDLVGILWILAQRSGLSTLAVMKK 165
QY 121 SSKFLPVIGSMWFSYFLERSWAKDESTLKGIOQLSDPFLPFWLALFVSGTRFTQAK 180
DB 166 SSKFLPVIGSMWFAEYLFERSWAKDEKTLKWLQRLKDFPRPFWLALFVSGTRFTPAK 225
QY 181 LLAQAEYATSTGLPVPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
DB 226 LLAQAEYASQGLPAPRNVLIPRTKGFVSANRDFVPAIYDVTIVPKDSPQPTMLRI 285
QY 241 FKQPSVVVHVIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
DB 286 LKGQSSVHVHRMKEHAMSEMPKSDDDVSKWCKDIFVTKDALLDKHLATGTF-DEEIRPTG 344
QY 301 RPKSLVVISWACLIVAGSVKFLQWSSLLSSWKGVAFAAGLAVVTALMQILLIOFSQSE 360
DB 345 RPKSLVLTFLWSCLLFLGAIEFFKWTQLLSTMRGVAFTRAGMALVTGVHVFVMSQAE 404
QY 361 RSNPAKIVPAKSKNK 375
DB 405 RSSAKAARNVEKKE 419

RESULT 10
US-09-970-989-5
Sequence 5, Application US/09970989
Patent No. US20020156262A1
GENERAL INFORMATION:
APPLICANT: LEUNG, David W.
APPLICANT: ADUREL, Daniel
APPLICANT: HOLLENBACK, David
TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
FILE REFERENCE: 077319/0151
CURRENT APPLICATION NUMBER: US/09/970,989
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/215,252
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: US 08/618,651
PRIOR FILING DATE: 1996-03-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5
LENGTH: 374
TYPE: PRT
ORGANISM: Maize
US-09-970-989-5

Query Match 75.0%; Score 1450.5; DB 9;
Best Local Similarity 70.7%; Pred. No. 9.4e-144;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPGLGILFFASGLLVNLQAICYVVRPVSKSLYRRINRVVAELLWL 60
DB 1 MAIPLVVLVPLGLLFLSGLVNAIQAVLFVTRPFKSLYRRINRFLAELLWLQVWV 60
QY 61 IDWAGVKVQIFTDHETFRMGKEHALVISNHRSDIDLVGVWSAQRSGCLSTLAVMKK 120
DB 61 VDWAGVKVQLHADEITYRSMGKEHALVISNHRSDIDLVGILWILAQRSGLSTLAVMKK 120
QY 121 SSKFLPVIGSMWFSYFLERSWAKDESTLKGIOQLSDPFLPFWLALFVSGTRFTQAK 180
DB 121 SSKFLPVIGSMWFAEYLFERSWAKDEKTLKWLQRLKDFPRPFWLALFVSGTRFTPAK 180
QY 181 LLAQAEYATSTGLPVPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
DB 181 LLAQAEYASQGLPAPRNVLIPRTKGFVSANRDFVPAIYDVTIVPKDSPQPTMLRI 240
QY 241 FKQPSVVVHVIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
DB 241 LKGQSSVHVHRMKEHAMSEMPKSDDDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPTG 299
QY 301 RPKSLVVISWACLIVAGSVKFLQWSSLLSSWKGVAFAAGLAVVTALMQILLIOFSQSE 360
DB 300 RPKSLVLTFLWSCLLFLGAIEFFKWTQLLSTMRGVAFTRAGMALVTGVHVFVMSQAE 359
QY 361 RSNPAKIVPAKSKNK 375
DB 360 RSSAKAARNVEKKE 374

RESULT 11
US-10-667-494-5
Sequence 5, Application US/10667494
Publication No. US20040043465A1
GENERAL INFORMATION:
APPLICANT: LEUNG, David W.
APPLICANT: ADUREL, DANIEL
APPLICANT: HOLLENBACK, DAVID
TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
FILE REFERENCE: 077319/0275
CURRENT APPLICATION NUMBER: US/10/667,494
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US/09/970,989A
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/215,252
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/618,651
PRIOR FILING DATE: 1996-03-19
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 374
TYPE: PRT
ORGANISM: Zea mays
US-10-667-494-5

Query Match 75.0%; Score 1450.5; DB 12; Length 374;
Best Local Similarity 70.7%; Pred. No. 9.4e-144;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPGLGILFFASGLLVNLQAICYVVRPVSKSLYRRINRVVAELLWL 60
DB 1 MAIPLVVLVPLGLLFLSGLVNAIQAVLFVTRPFKSLYRRINRFLAELLWLQVWV 60


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; Publication No. US20020007499A1
; GENERAL INFORMATION:
; APPLICANT: SLABAS, Antoni Ryszard
; APPLICANT: BROWN, Adrian Paul
; APPLICANT: BROUGH, Claire Louise
; APPLICANT: KROON, Johannes Theodorus Maria
; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT
; TITLE OF INVENTION: 2-ACYLTRANSFERASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,581B
; FILING DATE: March 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB96/00306
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: GB 9502468.3
; FILING DATE: 09-FEB-1995
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; US-08-818-581B-5

Query Match 74.5%; Score 1442.5; DB 8; Length 375;
Best Local Similarity 70.4%; Pred. No. 6.6e-143;
Matches 264; Conservative 51; Mismatches 59; Indels 1; Gaps 1;

Qy 1 MAIAAAVVPVLGLLFFASGLLVNLIQAICYVVVPVSKSLYRINRVVAELLMLLWL 60
Db 1 MAIPLVLVPLGLLFLSLGLIIVNAIQAVLFTVIRPFKSYRRINRFLAELLWLQLVV 60
Qy 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLGVWSAQRSGCLSTLAVMK 120
Db 61 VDWAGVKVQHAEETFRSMGKHALLIISNHRSDIDWLIGWILAQRSGCLSTLAVMK 120
Qy 121 SSKFLPVIGSMWPFSEYLFLEERSWAKDESTLKSQIQLSDPPLFWLALFVEGTRFTQAK 180
Db 121 SSKFLPVIGSMWFAEYLFLEERSWAKDEKTLKWGLQRLKDFPRPFMLALFVEGTRFTPAK 180
Qy 181 LLAQAEYATSTGLPVRNVLPRTKGFVSASHMRSFVPAIYDVTVVAIPKSSPAPTMRL 240
Db 181 LLAQAEYAASQGLPAPRNVLPRTKGFVSANVTIMEDFPAIYDVTVIIPKDSQPTMLRI 240
Qy 241 FKQPSVVVHVIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
Db 241 LKGQSSVHVHVKRHANSEMPKSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
Qy 301 RPKSLLVVISNACLIVAGSVKFLQWSLLSSWKGVAFSAGLAVVTALMQILIOFSQE 360
Db 300 RPKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWEGVAFAGMALVTVGMHVFIMFSQAE 359
Qy 361 RSNPAKIVPAKSKN 375
Db 360 RSSGARAARNVKE 374
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RESULT 15
US-10-437-963-130474
; Sequence 130474, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 130474
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_32632C.1.pap
; US-10-437-963-130474

Query Match 74.3%; Score 1438.5; DB 16; Length 374;
Best Local Similarity 72.1%; Pred. No. 1.7e-142;
Matches 264; Conservative 46; Mismatches 55; Indels 1; Gaps 1;

Qy 1 MAIAAAVVPVLGLLFFASGLLVNLIQAICYVVVPVSKSLYRINRVVAELLMLLWL 60
Db 1 MAVPLVLVPLGLLFLSLGLIIVNAIQAVLFLSIRPFKSLYRRINRFLAELLWLQLVL 60
Qy 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLGVWSAQRSGCLSTLAVMK 120
Db 61 VDWAGVKVQLHAEDETYKANGNEHALVISNHRSDIDWLIGWILAQRSGCLSTLAVMK 120
Qy 121 SSKFLPVIGSMWPFSEYLFLEERSWAKDESTLKSQIQLSDPPLFWLALFVEGTRFTQAK 180
Db 121 SSKFLPVIGSMWFAEYLFLEERSWAKDEKTLKWGLQRLKDFPRPFMLALFVEGTRFTPAK 180
Qy 181 LLAQAEYATSTGLPVRNVLPRTKGFVSASHMRSFVPAIYDVTVVAIPKSSPAPTMRL 240
Db 181 LLAQAEYAASQGLPAPRNVLPRTKGFVSANVTIMEDFPAIYDVTVIIPKDSQPTMLRI 240
Qy 241 FKQPSVVVHVIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
Db 241 LKGQSSVHVHVKRHANSEMPKSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
Qy 301 RPKSLLVVISNACLIVAGSVKFLQWSLLSSWKGVAFSAGLAVVTALMQILIOFSQE 360
Db 300 RPKSLLVTLFWSCLLLYGAVKLFVLTQLLSTWKGVGFTGLGLALVAVMHVFMFSQSE 359
Qy 361 RSNPAK 366
Db 360 RSSAK 365

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Sequence 128, App
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Sequence 3826, Ap
Sequence 5730, Ap
Sequence 22552, A
Sequence 133, App

28 303 15.7 354 4 US-09-218-207-74
29 242.5 12.5 228 3 US-09-338-907-70
30 242.5 12.5 228 4 US-09-218-207-70
31 219 11.3 315 3 US-09-338-907-134
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36 210.5 10.9 300 4 US-09-218-207-135
37 187.5 9.7 261 3 US-09-338-907-128
38 187.5 9.7 261 4 US-09-218-207-128
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40 174.5 9.0 185 4 US-09-218-207-136
41 160.5 8.3 346 4 US-09-252-991A-29402
42 157.5 8.1 319 4 US-09-540-236-3826
43 130.5 6.7 321 4 US-09-328-352-5730
44 130.5 6.7 364 4 US-09-252-991A-22552
45 129 6.7 182 3 US-09-338-907-133

ALIGNMENTS

RESULT 1
US-08-818-581B-4
; Sequence 4, Application US/08818581B
; Patent No. 6583340
; GENERAL INFORMATION:
; APPLICANT: SLABAS, Antoni Ryszard
; APPLICANT: BROWN, Adrian Paul
; APPLICANT: BROUGH, Clare Louise
; APPLICANT: KROON, Johannes Theodorus Maria
; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT
; TITLE OF INVENTION: 2-ACYLTRANSFERASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,581B
; FILING DATE: March 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB96/00306
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: GB 9502468.3
; FILING DATE: 09-FEB-1995
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-818-581B-4

Query Match 78.7%; Score 1523; DB 4; Length 377;
Best Local Similarity 77.3%; Pred. No. 1.2e-158;
Matches 283; Conservative 43; Mismatches 40; Indels 0; Gaps 0;
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Db 1 MAIPAAFTVPSLLFFMSGLVNFVQAVFYVLRPIKDTYRRINTLVAEELWLELWVW 60
QY 61 IDWAGVKVQITDHTFELMGKEHALVTSNHRSDIDLVGVWVSQORSCLGSLTAVMKK 120

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Title: US-09-914-098-56
Perfect score: 1935
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Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1450.5	75.0	374	2	US-08-454-267-2
3	1450.5	75.0	374	2	US-08-454-267-6
4	1450.5	75.0	374	2	US-08-941-319-2
5	1450.5	75.0	374	2	US-08-941-319-6
6	1450.5	75.0	374	3	US-09-035-098-2
7	1450.5	75.0	374	3	US-09-035-098-6
8	1450.5	75.0	374	4	US-09-215-252-5
9	1450.5	75.0	374	4	US-09-970-989A-5
10	1442.5	74.5	375	4	US-08-818-581B-5
11	1156.5	59.8	295	2	US-08-454-267-7
12	1156.5	59.8	295	2	US-08-941-319-7
13	1156.5	59.8	295	3	US-09-035-098-7
14	1156.5	59.8	311	4	US-08-818-581B-6
15	628	32.5	376	4	US-09-215-252-13
16	628	32.5	376	4	US-09-970-989A-13
17	534.5	28.7	378	4	US-09-215-252-17
18	534.5	28.7	378	4	US-09-970-989A-17
19	519.5	26.8	314	4	US-09-215-252-15
20	519.5	26.8	314	4	US-09-970-989A-15
21	304	15.7	353	3	US-08-996-306-4
22	304	15.7	353	3	US-09-338-907-4
23	304	15.7	353	4	US-09-218-207-4
24	304	15.7	364	2	US-08-996-306-5
25	304	15.7	364	3	US-09-338-907-5
26	304	15.7	364	4	US-09-218-207-5
27	303	15.7	354	3	US-09-338-907-74

61	IDWAGVKQLYDTT	ESFLMGKEHALI	CNHRSDIWLIGWLAQRCCGLSSIAVMKK	120
121	SKFETPVIGWSWMF	SEYILFLERSWAKOESTILKSGIORLSDP	PLPFWLALFVEGTRFTQAK	180
121	SSKFTLVIGWSWMF	SEYILFLERNWAKDENTILKSGLQRLNDF	PKPFWLALFVEGTRFTKAK	180
181	LAAAEYATSTGL	PVPRNVILPRTKGFVSASVHMRSPVPAI	YDVTVAIPKSSPAPTMURL	240
181	LAAAEYASAGL	PVPRNVILPRTKGFVSASVHMRSPVPAI	YDVTVAIPKSSPAPTMURL	240
241	FKGQSVVHVH	KRHLMKELPDDTDEAVAQWCRDIF	VAKDALLDKHMAEFTFSDQELQOTG	300
241	FRGKSSVVHVH	KRHLMKDLPKTDGVAQWCKQOF	ISKDALLDKHVAEDTFSGLEVDQIG	300
301	REPKSLVVVISWAC	LIVWAGSVKPELQWSLLSSWKGVAFSA	FGVLAVTALMQILIOFSSQSE	360
301	RPMKSLVVVISWAC	LIVWAGSVKPELQWSLLSSWKGVAFSA	FGVLAVTALMQILIOFSSQSE	360
361	RSNPAK	366		
361	HSTPAK	366		

RESULT 2

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US-08-454-267-2
; Sequence 2, Application US/08454267
; Patent No. 5843739
; GENERAL INFORMATION:
; APPLICANT: SLABAS, ANTONI R.
; APPLICANT: BROWN, ADRIAN P.
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,267
; FILING DATE: 08-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02528
; FILING DATE: 10-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-454-267-2

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Qy	61	IDNWAGVKVQI	FDTHETFLMGXKEHALVINSNHRSDIDWLNGWTSQAORSGLGSTLAWMK	120
Db	61	VDNWAGVKVQLH	ADDEETYSMGKEHALISNHRSDIDWLIGWLAQRSGLGSTLAWMK	120
Qy	121	SSKFLPVGWMSWFSEYLF	FLERSWAKDESLKSGIORLSDFPLPFMLAFVEGTRFTQAK	180
Db	121	SSKFLPVGWMSWFAEYLF	FLERSWAKDESLKWLQRLKDFPFMLAFVEGTRFTPAK	180
Qy	181	LAAQEWANSTGIPVRNVLI	PTKGFVSVMRSFVPAIYDVTVAIKSSSAPTWLRL	240
Db	181	LAAQEWASQGLPAPRNVLI	PTKGFVSVMIRDFVPAIYDVTIVPKDSQPTWLRI	240
Qy	241	FKQPSVWVYHIIKRHLMKEL	PDDEAVAQWCRDIFVAKDALLDKHAEGTFSQELODTG	300
Db	241	LKQSSVHVHVMKRRHAMSE	PKSDEVDVSKWCKDIFVAKDALLDKHLATGTF-DEETRPIG	299
Qy	301	RPTKSLLVISWACLVAAGSV	KFLQKSSLLSKWGAFSAGFLAVVTALMQLIOFSQSE	360
Db	300	RPVKSLLVTLFWSCLLFGA	IBFFKVTQLLUSTMRGVAFTAGNALVTGVNHEVTIMFSQAE	359
Qy	361	RSPNPAKIVPAKSQK	375	
Db	360	RSSSARAARNRVKKE	374	

RESULT 3

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US-08-454-267-6
; Sequence 6, Application US/08454267
; Patent No. 5843739
; GENERAL INFORMATION:
; APPLICANT: SLABAS, ANTONI R.
; APPLICANT: BROWN, ADRIAN P.
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,267
; FILING DATE: 08-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02528
; FILING DATE: 10-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-454-267-6

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Query Match	75.0%;	Score	1450.5;	DB 2;	Length	374;			
Best Local Similarity	70.7%;	Pred. No.	1.1e-150;						
Matches	265;	Conservative	51;	Mismatches	58;	Indels	1;	Gaps	1;
QY	1	MAIAAAVVVPLGLFPFAGGLVNLIIQATCYVVRPVSKSLYRINRVVAELIWLVL	60						
Db	1	MAIPLVVPLGLLFLLSGLIVNAIQALFVTRPFSKFYRRIIRFIAELLWLQLVWV	60						
QY	61	IDWAGVKVQITDTEHTRFLMGKEHALVLSNHRSDIDWLGVWVSAQRSGCGLSTLAVMKK	120						
Db	61	VDRWAGVKVQLHADBEYTSYMKKEHALIISNHRSDIDWLGIWLAQRSGCGLSTLAVMKK	120						
QY	121	SSKFLPVIGWSMWFYSYFLERSWAKDESTLKSIGIORLSDFFPLPFWLALFVEGTRFTQAK	180						
Db	121	SSKFLPVIGWSMWFAYEYFLERSWAKDEKTLKWLQRLKDFRPFWMALFVEGTRFTPAK	180						
QY	181	LLAAQAYATSTGLPVPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVVAIPKSSAPPTMLRL	240						
Db	181	LLAAQYAAASQGLPAPRNVLIPTKGFVSAVSIIMRDFVPAIYDVTIVPKDSQPMTMLRI	240						
QY	241	FKGQPSVWVHHIKRHLMKELPDTDEVAQWCROI FVAKDALLDKHNAEGTFSQEOLODTG	300						
Db	241	LKGQSSVTHVRMRHAMSEMPKSDDEPVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG	299						
QY	301	RPTKSLLVISMACLVAVAGSVKFLQWSLLSSMKGVAFSAFGLAVVATLMOILTFQSQSE	360						
Db	300	RPVKSLLVTLFWSCLLFGAIEIEFKTKQLLSTWEGVAFTAAGMALVTGVHVFIMFSQAE	359						
QY	361	RSNPAKIVPAKSNK	375						
Db	360	RSSSARAARNRVKE	374						

RESIST 5

US-08-941-319-6
 Sequence 6, Application US/08941319
 Patent No. 5945323
 GENERAL INFORMATION:
 APPLICANT: SLABAS, ANTONI R.
 APPLICANT: BROWN, ADRIAN P.
 TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: US
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/941,319
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/454,267
 FILING DATE: 08-JUN-1995
 APPLICATION NUMBER: PCT/GB93/02528
 FILING DATE: 10-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: REED, GRANT E.
 REGISTRATION NUMBER: P-41,264
 REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO. 6:
 SEQUENCE CHARACTERISTICS:

DES

LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-941-319-6

Query Match 75.0%; Score 1450.5; DB 2; Length 374;
Best Local Similarity 70.7%; Pred. No. 1.1e-150;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPGLGFFASGLLVNLIQAICVYVVRPVSKSLYRINRVVAELLWLEVL 60
DB 1 MAIPLVLVPLGLLFLSLGLVNAIQAVLFTVIRPFKSFYRINRFLAELLWLQVWV 60
QY 61 IDWAGVKVQIFTDHTFRLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMK 120
DB 61 VDWAGVKVQIHADEETYSRSGKEHALIISNHRSDIDWLIGWILAQRSGCLGSLTAVMK 120
QY 121 SSKFLPVIGSMWPFSEYLFELERSWAKDESTLKSIGIQLSDPFLPFWLALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWPAEYLFELERSWAKDEKTLKGLQRLKDFPPFWLALFVEGTRFTPAK 180
QY 181 LLAQEVATSTGLVPVRNVLIPRTKGFVSASVHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
DB 181 LLAQEVAAASQGLPAPRNVLIPRTKGFVSASVIMRDFVPAIYDVTIVPKDSPQPTMLRI 240
QY 241 FKGPSVVVHHIKHLMKELPDTDEAVAQCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
DB 241 LKGSSVHVHMRKHANSEPKSDESDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
QY 301 RPIKSLVWISWACLWVAGSVKFLQWSSLLSSMKGVAFSAFGLVAVTALMQILIQFSQE 360
DB 300 RPVKSLVTLVFWSCLLLFGAIEFFKQTLLSTWRGVAFTAGNALVTGVVHVFIMFSQAE 359
QY 361 RSNPAKIVPAKSNK 375
DB 360 RSSSARAARNRVKKE 374

RESULT 6

US-09-035-098-2
Sequence 2, Application US/09035098
Patent No. 6194640
GENERAL INFORMATION:
APPLICANT: SLABAS, ANTONI R.
APPLICANT: BROWN, ADRIAN P.
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,267
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT B. P-41,264
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-035-098-2

Query Match 75.0%; Score 1450.5; DB 3; Length 374;
Best Local Similarity 70.7%; Pred. No. 1.1e-150;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPGLGFFASGLLVNLIQAICVYVVRPVSKSLYRINRVVAELLWLEVL 60
DB 1 MAIPLVLVPLGLLFLSLGLVNAIQAVLFTVIRPFKSFYRINRFLAELLWLQVWV 60
QY 61 IDWAGVKVQIFTDHTFRLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMK 120
DB 61 VDWAGVKVQIHADEETYSRSGKEHALIISNHRSDIDWLIGWILAQRSGCLGSLTAVMK 120
QY 121 SSKFLPVIGSMWPFSEYLFELERSWAKDESTLKSIGIQLSDPFLPFWLALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWPAEYLFELERSWAKDEKTLKGLQRLKDFPPFWLALFVEGTRFTPAK 180
QY 181 LLAQEVATSTGLVPVRNVLIPRTKGFVSASVHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
DB 181 LLAQEVAAASQGLPAPRNVLIPRTKGFVSASVIMRDFVPAIYDVTIVPKDSPQPTMLRI 240
QY 241 FKGPSVVVHHIKHLMKELPDTDEAVAQCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
DB 241 LKGSSVHVHMRKHANSEPKSDESDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
QY 301 RPIKSLVWISWACLWVAGSVKFLQWSSLLSSMKGVAFSAFGLVAVTALMQILIQFSQE 360
DB 300 RPVKSLVTLVFWSCLLLFGAIEFFKQTLLSTWRGVAFTAGNALVTGVVHVFIMFSQAE 359
QY 361 RSNPAKIVPAKSNK 375
DB 360 RSSSARAARNRVKKE 374

RESULT 7

US-09-035-098-6
Sequence 6, Application US/09035098
Patent No. 6194640
GENERAL INFORMATION:
APPLICANT: SLABAS, ANTONI R.
APPLICANT: BROWN, ADRIAN P.
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,267
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT B. P-41,264
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
TELEPHONE: (202) 371-2600

```
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-035-098-6

Query Match          75.0%; Score 1450.5; DB 3; Length 374;
Best Local Similarity 70.7%; Pred. No. 1.1e-150;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLQAIQAVLVFTVIRPFKSFYRRINRFLAELLWLQVWV 60
DB 1 MAIPLVLVPLGLLFFASGLLVNLQAIQAVLVFTVIRPFKSFYRRINRFLAELLWLQVWV 60
DB 1 MAIPLVLVPLGLLFFASGLLVNLQAIQAVLVFTVIRPFKSFYRRINRFLAELLWLQVWV 60
QY 61 IDWAGVKVQIFDTHETFRMLGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120
DB 61 IDWAGVKVQIFDTHETFRMLGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120
DB 61 VDWAGVKVQLHADEETYSRMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120
QY 121 SSKFLPVIGSMWFMFSEYLFLEERSWAKDESTLKSGIORLSDFPLPFWALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWFMFSEYLFLEERSWAKDESTLKSGIORLSDFPLPFWALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWFMFSEYLFLEERSWAKDESTLKSGIORLSDFPLPFWALFVEGTRFTQAK 180
QY 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
DB 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
DB 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
QY 241 FKQPSVVVHHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELDTG 300
DB 241 FKQPSVVVHHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELDTG 300
DB 241 LKQSSVHVHVRKHAMSEPKSDEVDVSKCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
QY 301 RPIKSLVVISWACLAVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILLIQFSQSE 360
DB 301 RPIKSLVVISWACLAVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILLIQFSQSE 360
DB 300 RPKVSLVLTFLWSCLLLFGEIEFFKWTQLLSTWEGVAFVTAAGMALVTGVWHVFMFSQAE 359
QY 361 RSNPAKIVPAKSKNK 375
DB 361 RSNPAKIVPAKSKNK 375
DB 360 RSSSARAARNVKKE 374

RESULT 9
US-09-970-989A-5
; Sequence 5, Application US/09970989A
; Patent No. 6670143
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: ADUREL, DANIEL
; APPLICANT: HOLLENBACK, DAVID
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0275
; CURRENT APPLICATION NUMBER: US/09/970,989A
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/215,252
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-970-989A-5

Query Match          75.0%; Score 1450.5; DB 4; Length 374;
Best Local Similarity 70.7%; Pred. No. 1.1e-150;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLQAIQAVLVFTVIRPFKSFYRRINRFLAELLWLQVWV 60
DB 1 MAIPLVLVPLGLLFFASGLLVNLQAIQAVLVFTVIRPFKSFYRRINRFLAELLWLQVWV 60
DB 1 MAIPLVLVPLGLLFFASGLLVNLQAIQAVLVFTVIRPFKSFYRRINRFLAELLWLQVWV 60
QY 61 IDWAGVKVQIFDTHETFRMLGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120
DB 61 IDWAGVKVQIFDTHETFRMLGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120
DB 61 VDWAGVKVQLHADEETYSRMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120
QY 121 SSKFLPVIGSMWFMFSEYLFLEERSWAKDESTLKSGIORLSDFPLPFWALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWFMFSEYLFLEERSWAKDESTLKSGIORLSDFPLPFWALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWFMFSEYLFLEERSWAKDESTLKSGIORLSDFPLPFWALFVEGTRFTQAK 180
QY 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
DB 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
DB 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
QY 241 FKQPSVVVHHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELDTG 300
DB 241 FKQPSVVVHHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELDTG 300
DB 241 LKQSSVHVHVRKHAMSEPKSDEVDVSKCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
QY 301 RPIKSLVVISWACLAVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILLIQFSQSE 360
DB 301 RPIKSLVVISWACLAVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILLIQFSQSE 360
DB 300 RPKVSLVLTFLWSCLLLFGEIEFFKWTQLLSTWEGVAFVTAAGMALVTGVWHVFMFSQAE 359
QY 361 RSNPAKIVPAKSKNK 375
DB 361 RSNPAKIVPAKSKNK 375
DB 360 RSSSARAARNVKKE 374

RESULT 8
US-09-215-252-5
; Sequence 5, Application US/09215252
; Patent No. 6300487
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: ADUREL, Daniel
; APPLICANT: HOLLENBACK, David
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0151
; CURRENT APPLICATION NUMBER: US/09/215,252
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Maize
; US-09-215-252-5

Query Match          75.0%; Score 1450.5; DB 4; Length 374;
Best Local Similarity 70.7%; Pred. No. 1.1e-150;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLQAIQAVLVFTVIRPFKSFYRRINRFLAELLWLQVWV 60
DB 1 MAIPLVLVPLGLLFFASGLLVNLQAIQAVLVFTVIRPFKSFYRRINRFLAELLWLQVWV 60
DB 1 MAIPLVLVPLGLLFFASGLLVNLQAIQAVLVFTVIRPFKSFYRRINRFLAELLWLQVWV 60
QY 61 IDWAGVKVQIFDTHETFRMLGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120
DB 61 IDWAGVKVQIFDTHETFRMLGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120
DB 61 VDWAGVKVQLHADEETYSRMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120
QY 121 SSKFLPVIGSMWFMFSEYLFLEERSWAKDESTLKSGIORLSDFPLPFWALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWFMFSEYLFLEERSWAKDESTLKSGIORLSDFPLPFWALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWFMFSEYLFLEERSWAKDESTLKSGIORLSDFPLPFWALFVEGTRFTQAK 180
QY 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
DB 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
DB 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240
QY 241 FKQPSVVVHHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELDTG 300
DB 241 FKQPSVVVHHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELDTG 300
DB 241 LKQSSVHVHVRKHAMSEPKSDEVDVSKCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
QY 301 RPIKSLVVISWACLAVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILLIQFSQSE 360
DB 301 RPIKSLVVISWACLAVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILLIQFSQSE 360
DB 300 RPKVSLVLTFLWSCLLLFGEIEFFKWTQLLSTWEGVAFVTAAGMALVTGVWHVFMFSQAE 359
QY 361 RSNPAKIVPAKSKNK 375
DB 361 RSNPAKIVPAKSKNK 375
DB 360 RSSSARAARNVKKE 374
```

Db 241 LKQSSVHVVRKHAMSEPKSDSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299

QY 301 RPKISLLVVISWACLIVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMOILLIQFSQE 360

Db 300 RPKVSLVTLFWSCILLFLGAEFFKWTQLLSTWGVAFVTAAGMALVTGVMEVFIMFSQAE 359

QY 361 RSNPAKIVPAKSKNK 375

Db 360 RSSSARAARNRVKKE 374

RESULT 10

US-08-818-581B-5

; Sequence 5, Application US/08818581B

; Patent No. 6583340

; GENERAL INFORMATION:

; APPLICANT: SLABAS, Antoni Ryszard

; APPLICANT: BROWN, Adrian Paul

; APPLICANT: BROUGH, Clare Louise

; APPLICANT: KROON, Johannes Theodorus Maria

; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT

; TITLE OF INVENTION: 2-ACYLTRANSFERASE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: US

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (RPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/818,581B

; FILING DATE: March 14, 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB96/00306

; FILING DATE: 09-FEB-1996

; APPLICATION NUMBER: GB 9502468.3

; FILING DATE: 09-FEB-1995

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 375 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Zea mays

US-08-818-581B-5

Query Match 74.5%; Score 1442.5; DB 4; Length 375;

Best Local Similarity 70.4%; Pred. No. 8.4e-150;

Matches 264; Conservative 51; Mismatches 59; Indels 1; Gaps 1;

QY 1 MATAAAVVPGLGILFFASGLLVNLIQACVYVVRPVSKSLYRRINRVVAELLWELVWL 60

Db 1 MAIPLVLVLPGLGLLFLSGLIYNAIQVLFVTRPFSKSFYRRINRVFAELLWLQLVWV 60

QY 61 IDWAGVKVQIFDHTFTFLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120

Db 61 VDWAGVKVQLHADEITYSKGLHALIISNHRSDIDWLGIWLAQRSGCLGSLTAVMKK 120

QY 121 SSKFLPVIQSMWFSEYLFILERSWAKDESTLKSQIQLSDPFLPFWLALFVEGTRFTQAK 180

Db 121 SSKFLPVIQSMWFSEYLFILERSWAKDESTLKSQIQLSDPFLPFWLALFVEGTRFTPAK 180

QY 181 LIAAQYATSTGIPVRNVLIPTKGFVSAGVSHMSFVPAIYDVTVATPKSPAPTMLRL 240

Db 181 LIAAQYATSTGIPVRNVLIPTKGFVSAGVSHMSFVPAIYDVTVATPKSPAPTMLRI 240

QY 241 FKQSSVHVVRKHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTSDQELQDTG 300

Db 241 LKQSSVHVVRKHAMSEPKSDSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299

QY 301 RPKISLLVVISWACLIVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMOILLIQFSQE 360

Db 300 RPKVSLVTLFWSCILLFLGAEFFKWTQLLSTWGVAFVTAAGMALVTGVMEVFIMFSQAE 359

QY 361 RSNPAKIVPAKSKNK 375

Db 360 RSSSARAARNRVKKE 374

RESULT 11

US-08-454-267-7

; Sequence 7, Application US/08454267

; Patent No. 5843739

; GENERAL INFORMATION:

; APPLICANT: SLABAS, ANTONI R.

; APPLICANT: BROWN, ADRIAN P.

; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: US

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/454,267

; FILING DATE: 08-JUN-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB93/02528

; FILING DATE: 10-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: REED, GRANT E.

; REGISTRATION NUMBER: P-41,264

; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 295 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-454-267-7

Query Match 59.8%; Score 1156.5; DB 2; Length 295;

Best Local Similarity 61.4%; Pred. No. 1.5e-118;

Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;

QY 5 AAADVPLGLLFFASGLLVNLIQACVYVVRPVSKSLYRRINRVVAELLWELVWLIDWW 64

Db 4 AAADVPLGLLFFASGLLVNLI-----QKSGCLGSALAVMKSKSF 25

QY 65 AGVKVQIFDHTFTFLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKSKSF 124

Db 26 -----QKSGCLGSALAVMKSKSF 44

QY 125 LPVIGSMWFSEYLFILERSWAKDESTLKSQIQLSDPFLPFWLALFVEGTRFTQAKLLAA 184

Db 45 LPVIGSMWFSEYLFILERNWAKDESTLKSQIQLNDPFPFWLALFVEGTRFTQAKKAA 104

[illegible]

RESULT 12.

US-08-941-319-7
; Sequence 7, Application US/08941319
; Patent No. 5945323
; GENERAL INFORMATION:
; APPLICANT: SLABAS, ANTONI R.
; APPLICANT: BROWN, ADRIAN P.
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,319
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/454,267
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: PCT/GB93/02528
; FILING DATE: 10-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 0623.03.0000/JAG/GER
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-941-319-7

```

Query Match      59.8%; Score 1156.5; DB 2; Length 295;
Best Local Similarity 61.4%; Pred.No.1.5e-118;
Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;

QY 5 AAATVPLGLFFAFSGILVNLIOAICVVPVPSKSLYRINRVVAELNLJLVNLDMW 64
   AAAIVPLGLIFF:SGILVNL:
Db 4 AAAIVPLGLIFF:SGILVNL:----- 25

QY 65 AGVKYQVFTDHTETPRLMGKEHALVINSHRSDDWLVGWVSAQSRGCLGTLVAMKKSKF 124
   -----QSRGCLGSLAVNMKKSKSF 44
Db 26 -----

```

QY 65 AGVKQVFTDHTETRLMGKEHALVISNHRSDIDWLGVWSAQRSGCIGSTLAVMKKSKF 124
Db 26 -----QSGCIGSALAVMKKSKF 44
QY 125 LPVIGSMWFSEYFLERSWAKDESTLKSIGIQLSDPPLPFWLALFVEGTRFTQAKLAA 184
Db 45 LPVIGSMWFSEYFLERNWAKDESTLKSIGIQLSDPPLPFWLALFVEGTRFTQAKLAA 104
QY 185 QEVATSTGLPVRNVLPRTKGFVSAYSHMRSFVPALYDVTVAIPKSSPAPTMRLRPFKQ 244
Db 105 QEYASSELVPRNVLPRTKGFVSAYSHMRSFVPALYDVTVAIPKSSPAPTMRLRPFKQ 164
QY 245 PSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTGRPIK 304
Db 165 PSVVHVHIKCHSMKDLPESEDEIAQWCRDQFVTKDALLDKHIAADTFAGKEQNIQRPIK 224
QY 305 SLLVVISWACLVVAGSVKFLQWSLLSSWKGVAFAFGLAVVTALMQILIQFSQSERSNP 364
Db 225 SLAVVLSWACLLTLGAMKFLHNSLFSWKGIALSALGLGIITLQWILIRSSQSERSTP 284
QY 365 AKIVPAKSKN 374
Db 285 AKVAPAKPKD 294

RESULT 14
US-08-818-581B-6
; Sequence 6, Application US/08818581B
; Patent No. 6583340
; GENERAL INFORMATION:
; APPLICANT: SLABAS, Antoni Ryszard
; APPLICANT: BROWN, Adrian Paul
; APPLICANT: BROUGH, Claire Louise
; APPLICANT: KROON, Johannes Theodorus Maria
; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT
; TITLE OF INVENTION: 2-ACYLTRANSFERASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,581B
; FILING DATE: March 14, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB96/00306
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: GB 9502468.3
; FILING DATE: 09-FEB-1995
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Brassica napus
US-08-818-581B-6

Query Match 59.8%; Score 1156.5; DB 4; Length 311;
Best Local Similarity 61.4%; Pred. No. 1.7e-118;
Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;
QY 5 AAATVPLGLFFASGLLVNLQAIQCYVVRPVSKSLYRINRVVAELNLWELWLDWM 64

Db 4 AAATVPLGLFFASGLLVNL ----- 25
QY 65 AGVKQVFTDHTETRLMGKEHALVISNHRSDIDWLGVWSAQRSGCIGSTLAVMKKSKF 124
Db 26 -----QSGCIGSALAVMKKSKF 44
QY 125 LPVIGSMWFSEYFLERSWAKDESTLKSIGIQLSDPPLPFWLALFVEGTRFTQAKLAA 184
Db 45 LPVIGSMWFSEYFLERNWAKDESTLKSIGIQLSDPPLPFWLALFVEGTRFTQAKLAA 104
QY 185 QEVATSTGLPVRNVLPRTKGFVSAYSHMRSFVPALYDVTVAIPKSSPAPTMRLRPFKQ 244
Db 105 QEYASSELVPRNVLPRTKGFVSAYSHMRSFVPALYDVTVAIPKSSPAPTMRLRPFKQ 164
QY 245 PSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTGRPIK 304
Db 165 PSVVHVHIKCHSMKDLPESEDEIAQWCRDQFVTKDALLDKHIAADTFAGKEQNIQRPIK 224
QY 305 SLLVVISWACLVVAGSVKFLQWSLLSSWKGVAFAFGLAVVTALMQILIQFSQSERSNP 364
Db 225 SLAVVLSWACLLTLGAMKFLHNSLFSWKGIALSALGLGIITLQWILIRSSQSERSTP 284
QY 365 AKIVPAKSKN 374
Db 285 AKVAPAKPKD 294

RESULT 15
US-09-215-252-13
; Sequence 13, Application US/09215252
; Patent No. 6300487
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: ADOUREL, Daniel
; APPLICANT: HOLLEBACK, David
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0151
; CURRENT APPLICATION NUMBER: US/09/215,252
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-215-252-13
Query Match 32.5%; Score 628; DB 4; Length 376;
Best Local Similarity 37.6%; Pred. No. 2.7e-60;
Matches 127; Conservative 75; Mismatches 124; Indels 12; Gaps 4;
QY 12 LGLFFASGLLVNLQAIQCYVVRPVSKSLYRINRVVAELNLWELWLDWMWAGVKVQI 71
Db 17 VGFVVSGLVINPVQ-LCTLALWFSKQLYRRLNCLRLAYSLWSQLVMLLEWNSCTECL 75
QY 72 FTDHTETRLMGKEHALVISNHRSDIDWLGVWSAQRSGCIGSTLAVMKKSKFPLVIGWS 131
Db 76 FTDQATVERFGKEHAVIILNHNFEIDFLCGWTWCERFVLGSKVLAKELLYPLIGWT 135
QY 132 MWFSEYFLERSWAKDESTLKSIGIQLSDPPLPFWLALFVEGTRFTQAKLAAQEVATST 191
Db 136 WYFLEIVFCRKEEDRDTVVEGLRLSDYPEYMWFLYCEGTRFTETKRVSMEEVAAK 195
QY 192 GLPVRNVLPRTKGFVSAYSHMRSFVPALYDVTVAIPKSSPAPTMRLRPFKQSPVVHVH 251
Db 196 GLPYLKYHLLPRTKGFVTAVKCLRGTVAAVYDVTLNF-RGNKNPSLLGILYKGYEADM 254
QY 252 IKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTGRPIKSLLVVIS 311
Db 255 VRPEPLIEDIPLDEKAAQNLHKEYQKDLQELYNQKGMFPGSEQKPARP-WTLNLF 313

QY 312 WACLVVAGSVKFLQWSSLLSSWKGYAFSAFGLAVVTAL 349
Db 314 WATILL-----SPLFSVLGVFAFGSPLLLITFL 342

Search completed: July 7, 2004, 13:42:25
Job time : 24 secs

OM protein - protein search, using sw model

Run on: July 7, 2004, 13:33:02 ; Search time 59 Seconds
(without alignments)
1805.431 Million cell updates/sec

Title: US-09-914-098-56

Perfect score: 1935

Sequence: 1 MAIAAAVVPLGLFFASG.....QSERSNPAKIVPAKSKNGKS 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1935	100.0	377	AAB08478	Aab08478 Nucleotid
2	1609.5	83.2	387	AAy99482	Aay99482 Jojoba ac
3	1570	81.1	389	AAy99473	Aay99473 Arabidops
4	1570	81.1	389	AAg51310	Aag51310 Arabidops
5	1564	80.8	389	AAg13219	Aag13219 Arabidops
6	1504	77.7	377	AAr99249	Aar99249 Limnanthe
7	1453.5	75.1	360	AAg51330	Aag51330 Arabidops
8	1433.5	75.1	374	AAr59712	Aar59712 Maize 2-a
9	1450.5	75.0	374	AAU00667	Aau00667 Maize lys
10	1450.5	75.0	374	AAE15288	Aae15288 Maize LPA
11	1431.5	74.0	374	AAAB08477	Aab08477 Amino aci
12	1414.5	73.1	374	AAAB08479	Aab08479 Amino aci
13	1277	66.0	376	AAAg31583	AAg31583 Arabidops
14	1246	64.4	310	AAAg31311	AAg31311 Arabidops
15	1240	64.1	310	AAg13220	AAg13220 Arabidops
16	1155.5	59.7	294	AAg33441	AAg33441 Zea mays
17	1147.5	59.3	295	AAr59713	AAr59713 Rapessed
18	1129.5	58.4	281	AAAg31331	AAg31331 Arabidops
19	1068	55.2	273	AAAg31312	AAg31312 Arabidops
20	1062	54.9	273	AAg13221	AAg13221 Arabidops
21	967.5	50.0	257	AAg33442	AAg33442 Zea mays
22	958.5	49.5	240	AAb75581	Aab75581 Gene 29 h
23	951.5	49.2	240	AAAg31332	AAg31332 Arabidops
24	893.5	46.2	243	AAg33443	AAg33443 Zea mays
25	889	45.9	273	AAg31584	AAg31584 Arabidops

26	836	43.2	259	3	AAg31585	AAg31585 Arabidops
27	628	32.5	353	4	AAm39793	Aam39793 Human pol
28	628	32.5	368	3	AAy99422	Aay99422 Human PRO
29	628	32.5	368	4	AAb66171	Aab66171 Protein c
30	628	32.5	368	4	AAU29192	Aau29192 Human PRO
31	628	32.5	368	6	ABU58568	Abu58568 Human PRO
32	628	32.5	368	6	ABU88116	Abu88116 Novel hum
33	628	32.5	368	6	ABU84431	Abu84431 Human sec
34	628	32.5	368	6	ABR66305	AbR66305 Human sec
35	628	32.5	368	6	ABR65695	AbR65695 Human sec
36	628	32.5	368	6	ABU99635	AbU99635 Human sec
37	628	32.5	368	6	ABU82874	AbU82874 Human PRO
38	628	32.5	368	6	ABU99995	AbU99995 Novel hum
39	628	32.5	368	6	ABR68244	AbR68244 Human sec
40	628	32.5	368	6	ABU96297	AbU96297 Novel hum
41	628	32.5	368	6	ABU92728	AbU92728 Human sec
42	628	32.5	368	6	ABO08805	ABO08805 Human sec
43	628	32.5	368	6	ABO02857	ABO02857 Human sec
44	628	32.5	368	6	ABR75011	AbR75011 Human sec
45	628	32.5	368	6	ABR94773	AbR94773 Human sec

ALIGNMENTS

RESULT 1

AA08478

ID AAB08478 standard; protein; 377 AA.

XX

AC AAB08478;

XX

DT 20-DEC-2000 (first entry)

XX

DE Nucleotide sequence of a lysophosphatidic acid acetyltransferase.

XX

KW Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;

KW triacylglycerol; oil content.

XX

OS Glycine max.

XX

PN WO200049156-A2.

XX

PD 24-AUG-2000.

XX

PF 22-FEB-2000; 2000WO-US004526.

XX

PR 22-FEB-1999; 99US-0121119P.

XX

(DUPO) DU PONT DE NEMOURS & CO E I.

PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ, Ripp KG;

XX

WPI; 2000-558300/51.

DR N-PSDB; AAA64200.

XX

PT New nucleic acid fragment encoding a lysophosphatidic acid acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants which encode LPAAT at higher or lower levels than normal.

XX

PS Claim 31; Page 99-100; 102pp; English.

XX

CC The present sequence represents a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes

XX

SQ Sequence 377 AA;

Query Match 100.0%; Score 1935; DB 3; Length 377;
 Best Local Similarity 100.0%; Pred. No. 4e-194;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIAAAVVPGLGILFFASGLLVNLIQAICVTVVPVSKSLYRINRVVAELLMLELWL 60
 DB 1 MAIAAAVVPGLGILFFASGLLVNLIQAICVTVVPVSKSLYRINRVVAELLMLELWL 60

QY 61 IDWAGVKVQIFTDHTFRLMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 120
 DB 61 IDWAGVKVQIFTDHTFRLMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 120

QY 121 SSKFLPVIGSMWFSEYLFLEERSWAKDESTLKSGIQLSDFFLPFWLALFVEGTRFQAK 180
 DB 121 SSKFLPVIGSMWFSEYLFLEERSWAKDESTLKSGIQLSDFFLPFWLALFVEGTRFQAK 180

QY 181 LLAQEVATSTGLPVRNVLIPRTKGFVSASHMRSEFVPAIYDVTVAIPKSSPAPTMRL 240
 DB 181 LLAQEVATSTGLPVRNVLIPRTKGFVSASHMRSEFVPAIYDVTVAIPKSSPAPTMRL 240

QY 241 FKGPSPVHVHVKHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
 DB 241 FKGPSPVHVHVKHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300

QY 301 RPIKSLLVISWACLTVAGSVKFLQSSLLSSKGVAFSAFGLAVVTALMQILIQFSQSE 360
 DB 301 RPIKSLLVISWACLTVAGSVKFLQSSLLSSKGVAFSAFGLAVVTALMQILIQFSQSE 360

QY 361 RSNPAKIVPAKSNKGS 377
 DB 361 RSNPAKIVPAKSNKGS 377

RESULT 2
 AAY99482
 ID AAY99482 standard; protein; 387 AA.
 XX
 AC AAY99482;
 XX
 DT 15-AUG-2000 (first entry)
 XX
 DE Jojoba acyltransferase LPAAT, SEQ ID NO:162.
 XX
 KW Lysophosphatidic acid acyltransferase; LPAAT; jojoba; lipid synthesis;
 KW recombinant expression; membrane fluidity; cold resistance;
 XX transgenic plant.
 XX
 OS Simmondsia chinensis.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 40
 FT /note= "Encoded by NNTACA"
 XX
 XX WO200018889-A2.
 XX
 XX 06-APR-2000.
 XX
 XX 24-SEP-1999; 99WO-US022231.
 XX
 XX 25-SEP-1998; 98US-0101939P.
 XX
 XX (CALJ) CALGENE LLC.
 XX
 XX Lassar MW, Emig RA, Ruezinsky DM, Van Benennaam A;
 XX WPI; 2000-303447/26.
 DR N-P8DB; AAA37472.
 XX
 XX Novel acyltransferase related proteins useful for altering membrane
 PT fluidity in plant cells e.g. to induce chill tolerance.
 XX
 XX

PS XX
 CC The invention relates to nucleic acids encoding novel plant
 CC acyltransferase-like proteins (AAA37443-A37445) which comprise one of 8
 CC conserved acyltransferase motifs (AA99474-99481). Acyltransferases
 CC catalyze the transfer of acyl groups from a donor to a variety of
 CC substrates such as glycerides, steroids, stanols and phosphatides. Such
 CC enzymes play a key role in lipid synthesis, and thereby affect the
 CC characteristics of the plant. For example, cold-hardened plants have
 CC different lipid concentrations in the cell membrane compared to non-
 CC hardened plants, which makes the membrane more fluid and the plant more
 CC tolerant of low temperatures. The nucleic acid sequences of the invention
 CC can be used as probes or for expressing acyltransferase-like proteins in
 CC host cells e.g., for recombinant protein production. They may be
 CC expressed in plant cells to alter the lipid composition of the plant
 CC e.g., for the production of chill-resistant plants, or for altering the
 CC composition of plant oils. The present sequence represents jojoba
 CC lysophosphatidic acid acyltransferase (LPAAT)

QY 1 MAIAAAVVPGLGILFFASGLLVNLIQAICVTVVPVSKSLYRINRVVAELLMLELWL 60
 DB 1 MGIPAAAVIVPGLGILFFGSLFINFIOAICFVLRPLSKT-YRINRVVLELLELWL 59

QY 61 IDWAGVKVQIFTDHTFRLMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 120
 DB 60 VDWAASVKIKLFTDPDIFRLMGKEHALVISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 119

QY 121 SSKFLPVIGSMWFSEYLFLEERSWAKDESTLKSGIQLSDFFLPFWLALFVEGTRFQAK 180
 DB 120 SSKFLPVIGSMWFSEYLFLEERSWAKDESTLKSGIQLSDFFLPFWLALFVEGTRFQAK 179

QY 181 LLAQEVATSTGLPVRNVLIPRTKGFVSASHMRSEFVPAIYDVTVAIPKSSPAPTMRL 240
 DB 180 LLAQEVATSTGLPVRNVLIPRTKGFVSASHMRSEFVPAIYDVTVAIPKSSPAPTMRL 239

QY 241 FKGPSPVHVHVKHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
 DB 240 FKGPSTVHVHVKHMRSMKDLPEAADVAQWCRDIFVAKDALLDKHNVDDTFFGDEYLQDTG 299

QY 301 RPIKSLLVISWACLTVAGSVKFLQSSLLSSKGVAFSAFGLAVVTALMQILIQFSQSE 360
 DB 300 RPKSLFVAVSWALILGLGKFLRWSSLLSSKGVAFSAACLVLTILMQILIQFSQSE 359

QY 361 RSNPAKIVPAKSNK 374
 DB 360 RSTPAKVAPGPKN 373

RESULT 3
 AAY99473
 ID AAY99473 standard; protein; 389 AA.
 XX
 AC AAY99473;
 XX
 DT 15-AUG-2000 (first entry)
 XX
 DE Arabidopsis thaliana acyltransferase ATLPAAT1.
 XX
 KW Lysophosphatidic acid acyltransferase; ATLPAAT1; lipid synthesis;
 KW recombinant expression; membrane fluidity; cold resistance;
 XX transgenic plant.
 XX
 OS Arabidopsis thaliana.
 XX
 XX WO200018889-A2.
 XX

XX	24-SEP-1999;	99WO-US022231.	
XX	PP		
XX	PR		
XX	25-SEP-1998;	98US-0101939P.	
XX	PA	(CALJ) CALGENE LLC.	
XX	PI		
XX	Lassner MW, Emig RA, Ruezinsky DM, Van Eenennaam A;		
XX	WPI; 2000-303447/26.		
XX	N-PSDB; AAA37342.		
XX	Novel acyltransferase related proteins useful for altering membrane		
PT	fluidity in plant cells e.g. to induce chill tolerance.		
XX	Example 5; Page 75-76; 126pp; English.		
XX	The invention relates to nucleic acids encoding novel plant		
XX	acyltransferase-like proteins (AAA37343-A37445) which comprise one of 8		
CC	conserved acyltransferase motifs (AAAY99474-Y99481). Acylttransferases		
CC	catalyse the transfer of acyl groups from a donor to a variety of		
CC	substrates such as glycerides, sterols, stanols and phosphatides. Such		
CC	enzymes play a key role in lipid synthesis, and thereby affect the		
CC	characteristics of the plant. For example, cold-hardened plants have		
CC	different lipid concentrations in the cell membrane compared to non-		
CC	hardened plants, which makes the membrane more fluid and the plant more		
CC	tolerant of low temperatures. The nucleic acid sequences of the invention		
CC	can be used as probes or for expressing acyltransferase-like proteins in		
CC	host cells e.g., for recombinant protein production. They may be		
CC	expressed in plant cells to alter the lipid composition of the plant		
CC	e.g., for the production of chill-resistant plants, or for altering the		
CC	composition of plant oils. Sequences AAAY99463-Y99473 represent cDNAs		
CC	encoding Arabidopsis thaliana acyltransferases ATAT1-ATAT4, ATAT6-ATAT11		
CC	and lysophosphatidic acid acyltransferase ATLPAAT1, respectively		
XX	Sequence 389 AA;		
XX			
XX	Query Match	81.1%; Score 1570; DB 3; Length 389;	
XX	Best Local Similarity	77.2%; Pred. No. 9.2e-156;	
XX	Matches	287; Conservative 43; Mismatches 42; Indels 0; Gaps 0;	
QY	3	IAAAAVVPLGLLEFFASGLLVNLQATCYVVVVRVPSKSLYRINRVVAELIWLVLID 62	
DB	2	VIAAAVIVPLGLLEFFISGLAVNLQFQVCYVLRSLKNTYRKINRVVAELIWLVLVID 61	
QY	63	WWAGVKQVIFDHTDFTFLMGKEHALVINSNHRSDIDLWVGWVSQAQRSGCLSTLAWMKSS 122	
DB	62	WWAGVKIQVFADNTEFFEMGKEHALVVCNHRSDIDLWVGWTLAQRSGCLSGALAWMKSS 121	
QY	123	KFLPVIGSMWFSEYLFLERWAKDESTLKSIGIQELSDFFLPFPFWALFVEGTRTQAKLL 182	
DB	122	KFLPVIGSMWFSEYLFLERWAKDESTLKSGLQRLSDFFPPFWALFVEGTRTEAKLK 181	
QY	183	AAQEVATSTGLVPNRNVLIPRTKGFVSAVSNMRSFVPAIYDVTVVAIPKSSDPATMLRFK 242	
DB	182	AAQEVAASELIPINRVLIPRTKGFVSAVSNMRSFVPAIYDVTVTIPTKSPPTMLRFK 241	
QY	243	GQPSVVVHVHVKHLMKELPDTDEAVAQWCRI FVAKDALLDKHNAEGTFSQETQDTRP 302	
DB	242	GQPSVVVHVHVKCHSMKDLPESDAIAQWCRDQFVAKDALLDKHIAADTFPGQCFQNIQRP 301	
QY	303	IKSLILVITSWACLVAGSVKFLQWSGLLSSWKGVAFSAFGLAVVTALMOILLIQFSQSERS 362	
DB	302	IKSLAVLITSWACVLTLTGAIKFLHWAQLFSSWKGITISALGLIITLCMQILLIRSQSERS 361	
QY	363	NPAKIVPAKSKN 374	
DB	362	TPAKVVPAPKD 373	
RESULT 4			
AAG51310			
ID	AAG51310 standard; protein; 389 AA.		

PR	18-JUN-1999;	99US-0139462P.	PR	25-AUG-1999;	99US-0150566P.
PR	18-JUN-1999;	99US-0139463P.	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151065P.
PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151066P.
PR	21-JUN-1999;	99US-0139817P.	PR	30-AUG-1999;	99US-0151080P.
PR	22-JUN-1999;	99US-0139893P.	PR	31-AUG-1999;	99US-0151303P.
PR	23-JUN-1999;	99US-0140353P.	PR	01-SEP-1999;	99US-0151438P.
PR	23-JUN-1999;	99US-0140354P.	PR	07-SEP-1999;	99US-0151930P.
PR	24-JUN-1999;	99US-0140695P.	PR	10-SEP-1999;	99US-0152363P.
PR	28-JUN-1999;	99US-0140823P.	PR	13-SEP-1999;	99US-0153070P.
PR	29-JUN-1999;	99US-0140991P.	PR	15-SEP-1999;	99US-0153758P.
PR	30-JUN-1999;	99US-0141287P.	PR	16-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	99US-0141842P.	PR	20-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	PR	22-SEP-1999;	99US-0154779P.
PR	02-JUL-1999;	99US-0142055P.	PR	23-SEP-1999;	99US-0155139P.
PR	06-JUL-1999;	99US-0142330P.	PR	24-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	28-SEP-1999;	99US-0156559P.
PR	09-JUL-1999;	99US-0142920P.	PR	29-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	04-OCT-1999;	99US-0157117P.
PR	13-JUL-1999;	99US-0143542P.	PR	05-OCT-1999;	99US-0157753P.
PR	14-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	15-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144894P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144814P.	PR	21-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145192P.	PR	22-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160880P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0160989P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161405P.
PR	28-JUL-1999;	99US-0145919P.	PR	25-OCT-1999;	99US-0161406P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161359P.
PR	02-AUG-1999;	99US-0146388P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146389P.	PR	26-OCT-1999;	99US-0161361P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161920P.
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161922P.
PR	04-AUG-1999;	99US-0147302P.	PR	28-OCT-1999;	99US-0161933P.
PR	05-AUG-1999;	99US-0147319P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147260P.			
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.			
PR	09-AUG-1999;	99US-0147493P.			
PR	09-AUG-1999;	99US-0147935P.			
PR	10-AUG-1999;	99US-0148171P.			
PR	11-AUG-1999;	99US-0148319P.			
PR	12-AUG-1999;	99US-0148341P.			
PR	13-AUG-1999;	99US-0148565P.			
PR	13-AUG-1999;	99US-0148684P.			
PR	16-AUG-1999;	99US-0149368P.			
PR	17-AUG-1999;	99US-0149175P.			
PR	18-AUG-1999;	99US-0149426P.			
PR	20-AUG-1999;	99US-0149722P.			
PR	20-AUG-1999;	99US-0149723P.			
PR	20-AUG-1999;	99US-0149929P.			
PR	23-AUG-1999;	99US-0149902P.			
PR	23-AUG-1999;	99US-0149930P.			

Query Match 81.1%; Score 1570; DB 3; Length 389;
 Best Local Similarity 77.2%; Pred. No. 9.2e-156;
 Matches 287; Conservative 43; Mismatches 42; Indels 0; Gaps 0;

Qy	3	IAAAVVPVPLGLFFASGLLVNLIQAVVVPVSKSLYRRNRYVALLMLELVLLID 62
Db	2	VIAAAVVPVPLGLFFISGLAVNLFOAVCYVLRPISKNYRKINRYVATLWELVWVD 61
Qy	63	WVAGVKVQFTDTHETFLMGKEHALVSNHRSDIDWLVGVSAQSGCLGSLTAVNKKSS 122
Db	62	WVAGVKIQVFADNETFNRMGKEHALVVCNHRSDIDWLVGMILAQRSGCLGSALAVNKKSS 121
Qy	123	KFLPVIQWSMWFSEYLFLEERSWAKDESLTKSGIQRISDFLPFWLALFVEGTRFTQAKLL 182
Db	122	KFLPVIQWSMWFSEYLFLEERNWAKDESLTKSGIQRISDFLPFWLALFVEGTRFTQAKLL 181
Qy	183	AQOEYATSTGLPVRNVLIPRTKGFVSASHVRSFVPAIDYVTVAIQKSSPAPTMLRLFK 242

Qy	243	QPSVVVHHIKHRLMKELPDTDEAVAQCRDIFVAKDALLDKHMAEGTFSQDELQDTGRP	302	04-JUN-1999;
Ddb	242	QPSVVVHHIKCHSKMDLPESDDAIAQWCRDQFVAKDALLDKHIAADTFPGQEQNIGRP	301	07-JUN-1999;
Qy	303	IKSLIVVSWACLVVAGSVKFLQNSILLSSNKGVAFAFLAVVTALMQILLIQFSQSRS	362	08-JUN-1999;
Ddb	302	IKSLAVVSWACVLTGAIKFLHWAQLFSSWKGGITISALGLUIGITLCMQILLIRSQSRS	361	10-JUN-1999;
Qy	363	NPAKIVPAKSKN 374		14-JUN-1999;
Db	362	TPAKVPAKPKD 373		16-JUN-1999;
				17-JUN-1999;
				18-JUN-1999;
				19-JUN-1999;
				20-JUN-1999;
				21-JUN-1999;
				22-JUN-1999;
				23-JUN-1999;
				24-JUN-1999;
				25-JUN-1999;
				26-JUN-1999;
				27-JUN-1999;
				28-JUN-1999;
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				30-JUN-1999;
				01-JUL-1999;
				02-JUL-1999;
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				16-JUL-1999;
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				25-JUL-1999;
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				15-AUG-1999;
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				28-SEP-1999;
				29-SEP-1999;
				30-SEP-1999;
				01-OCT-1999;
				02-OCT-1999;
				03-OCT-1999;
				04-OCT-1999;
</				

PT improved oil prodn.
XX
XX Example 2; Fig 1; 54pp; English.
XX
CC The amino acid sequence (AAR99249) was deduced of Limnanthes clone 1
CC (AAR3205), a cDNA clone obtd. by heterologous screening of a Limnanthes
CC douglasii seed cDNA library using a 600 bp NcoI/PstI fragment of a rape 2
CC acyltransferase (2AR) clone corresponding to the N-terminus of the rape
CC protein. Another isolated clone (AAR3204) codes for Limnanthes 2AR
CC (AAR99248), which can be used to increase the erucic acid content of
CC transgenic plants
XX
XX Sequence 377 AA;
SQ

Query Match 77.7%; Score 1504; DB 2; Length 377;
Best Local Similarity 76.2%; Pred. No. 7.5e-149;
Matches 279; Conservative 45; Mismatches 42; Indels 0; Gaps 0;

QY 1 MAIAAAVVPVGLLFFAGSLVNLQAIQYVVVRPVSKSLYRINRVVAELLWLELVL 60
DB 1 MAIPAAAFVPISLFFMGLVNVFIQAVFYVLRPISKDYRINTLVAELLWLELVLV 60

QY 61 IDWAGVKVQIFDTHETFLMKKEHALVINSRSDIDWLVGVWSAQRSCGLSTLAVMKK 120
DB 61 IDWAGVKVQLYDTEFSLMRKEHALICNHRSDIDWLVGVWSAQRSCGLSSIAVMKK 120

QY 121 SSKFLVIGSMWFSEYLFERSWAKDESTLKSQIQLSDFFLPFWLALFVEGTRPTOK 180
DB 121 SSKFLVIGSMWFSEYLFERNWAKDENTLKSGLQRLNDFPKFWLALFVEGTRFTAK 180

QY 181 LLAQSYATSTGLPVRPNVLPRTKGFVSASVHMSRFSVPAIYDVTVVAIPKSPAPTMURL 240
DB 181 LLAQSYAASAGLPVRPNVLPRTKGFVSASVHMSRFSVPAIYDLTVVAIPKTEQPTMURL 240

QY 241 FKQPSVHVHKEHLMKELPDDEAVAQWCRDIFVAKDALLDKMAEGTFSDOELQDTG 300
DB 241 FRKSSVHVHLKRHLMKDFFPKTDDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVDIG 300

QY 301 RPIKSLVIVTSWACLVAAGSVKFLQWSLLSSKGVAFSAFGLVAVTALMQILIQFSQSE 360
DB 301 RPKSLVIVVSNWCLLGLVKFLQWSALLSSKGMWITTFVLGIVTALMHLIRSSQSE 360

QY 361 RSNPAK 366
DB 361 HSTPAK 366

RESULT 7
AAG51330
ID AAG51330 standard; protein; 360 AA.
XX
XX AAG51330;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65137.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
PN EF1033405-A2.
XX
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126254P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139482P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142053P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.

DE Maize 2-acyltransferase.

XX 2-Acyltransferase; lipid; oilseed; Escherichia coli; transgenic plant;

KW crop improvement.

XX Zea mays.

OS WO9413814-A1.

XX 23-JUN-1994.

XX 10-DEC-1993; 93WO-GB002528.

XX 10-DEC-1992; 92GB-00025845.

XX (NICK-) NICKERSON BIOCHEM LTD.

XX Slabas AR, Brown AP;

PI WPI; 1994-217888/26.

DR N-PSDB; AAQ68267.

XX DNA encoding a plant 2-acyl-transferase - used to produce plants with

PT increased or decreased lipid levels and with a tailored lipid compen.

XX Disclosure; Fig 1; 45pp; English.

XX Complementation studies using a maize cDNA library transferred into E.

CC coli JC201 allowed the isolation of a plasmid encoding a 2-

CC acyltransferase enzyme from maize. DNA encoding 2-acyltransferase can be

CC used to produce transgenic plants having altered lipid contents. (Updated

CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct

CC PA field.)

XX Sequence 374 AA;

XX Query Match 75.1%; Score 1453.5; DB 2; Length 374;

XX Best Local Similarity 70.9%; Pred. No. 1.5e-143;

XX Matches 266; Conservative 50; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRINRVVAELLWLEVL 60

DB 1 MAIPLVLVPLGLLFLSLGLVNAIQAVLFTIRPFPSFYRRINRFLAELLWLELVV 60

QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDLWVGWVSAQRSGCLGSTLAVMKK 120

DB 61 VDWAGVKVQLHADETYRSMGKEHALIISNHRSDIDLWIGLAQRSGCLGSTLAVMKK 120

QY 121 SSKFLPVIGWMMWFSEYLFLEERSWAKDESTLKSIGIQRSLDPPFPWALFVEGTRFTQAK 180

DB 121 SSKFLPVIGWMMWFAEYLFLEERSWAKDEKTLKWGLQRLKDFPRFPWALFVEGTRFTPAK 180

QY 181 LLAAQEVATSTGLPVPRNVLIPTKGFVSASVSHMRGFPVPAIYDVTVAIPKSSPAPTMLRL 240

DB 181 LLAAQEVAAASQGLPAPRNVLIPRTKGFVSASVIMRDFVPAIYDVTIVPKDSPQPTMLRI 240

QY 241 FKQPSVVVHHIKRHLMKELPDTDEAVAQWCRI FVAKDALLDKHMAAGTFSQDELQDTG 300

DB 241 LKGQSVIHVMRKRHAMSEPKSDEDEYKWKCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299

QY 301 RPKLSLAVIWSACLVLVAGSVKFLQKSSLLSKWGVAFSAFGLAVVTALMQILIOFSQSE 360

DB 300 RPVKSLLVTLFWSCLLLFGAIEFFKTLQLLSTWRGVAFTAGMALVTGVNHFIMFSQAE 359

QY 361 RSNPAKIVPAKSKNK 375

DB 360 RSSSARAARNRVKE 374

RESULT 9

AAU00667

ID AAU00667 standard; protein; 374 AA.

XX

AC AAU00667;

XX 07-SEP-2001 (first entry)

XX Maize lysophosphatidic acid acyltransferase (LPAAT).

XX Lysophosphatidic acid acyltransferase epsilon; LPAAT-epsilon; LPA; PA;

KW lysophosphatidic acid; phosphatidic acid; acylation; cellular activation;

KW phospholipid signalling; mitogenesis; inflammation; autoimmune disease;

KW oncology; cancer; obesity; gene therapy; maize.

XX Zea sp.

OS WO200134782-A1.

XX 17-MAY-2001.

XX 02-NOV-2000; 2000WO-US030193.

XX 09-NOV-1999; 99US-00436919.

XX (CELL-) CELL THERAPEUTICS INC.

XX Leung DW;

XX WPI; 2001-335920/35.

XX Novel isolated human isoform of lysophosphatidic acid acyltransferase-

PT epsilon useful for diagnostic, therapeutic and screening purposes.

XX Example 1; Fig 2; 48pp; English.

XX The sequence represents a maize lysophosphatidic acid acyltransferase

CC (LPAAT) isoform, LPAAT-delta, similar to a human LPAAT isoform, LPAAT-

CC epsilon. LPAAT catalyses the acylation of lysophosphatidic acid (LPA) to

CC phosphatidic acid (PA). LPA and PA have been identified as phospholipid

CC signalling molecules that affect a wide range of biological responses. PA

CC is involved in cellular activation and mitogenesis. Compounds that block

CC PA generation and hence diminish lipid biosynthesis and the signal

CC involved in cell activation are of therapeutic interest in the areas of

CC inflammation and oncology (e.g. autoimmune diseases and cancer) as well

CC as obesity treatment. LPAAT-epsilon and its corresponding DNA can be used

CC in screening assays to detect agents that stimulate or inhibit the

CC activity of LPAAT and, therefore, PA. The DNA is useful in tests to

CC detect the presence or expression of LPAAT-epsilon in relation to certain

CC diseases and conditions, and in disease prevention and treatment. The

CC sequences of the invention are also useful for diagnosis of diseases and

CC conditions in which the expression of LPAAT enzyme is abnormal

XX Sequence 374 AA;

XX Query Match 75.0%; Score 1450.5; DB 4; Length 374;

XX Best Local Similarity 70.7%; Pred. No. 3.1e-143;

XX Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRINRVVAELLWLEVL 60

DB 1 MAIPLVLVPLGLLFLSLGLVNAIQAVLFTIRPFPSFYRRINRFLAELLWLELVV 60

QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDLWVGWVSAQRSGCLGSTLAVMKK 120

DB 61 VDWAGVKVQLHADETYRSMGKEHALIISNHRSDIDLWIGLAQRSGCLGSTLAVMKK 120

QY 121 SSKFLPVIGWMMWFSEYLFLEERSWAKDESTLKSIGIQRSLDPPFPWALFVEGTRFTQAK 180

DB 121 SSKFLPVIGWMMWFAEYLFLEERSWAKDEKTLKWGLQRLKDFPRFPWALFVEGTRFTPAK 180

QY 181 LLAAQEVATSTGLPVPRNVLIPTKGFVSASVSHMRGFPVPAIYDVTVAIPKSSPAPTMLRL 240

DB 181 LLAAQEVAAASQGLPAPRNVLIPRTKGFVSASVIMRDFVPAIYDVTIVPKDSPQPTMLRI 240

QY 241 FKQPSVVVHHIKRHLMKELPDTDEAVAQWCRI FVAKDALLDKHMAAGTFSQDELQDTG 300

Db 241 LKQSSVHVHRMKGHAMSEMPKSDSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
Qy 301 RPIKSLVWISWACLWVAGSVKFLQSSLLSSWKGVAFAFGLAVVTALMQILTIQFSQSE 360
Db 300 RPKVSLVTVFWSCLLLFGLAIEFEKWTQLLSTWRGVAFAGMALVTGVHVFIMFSQAE 359
Qy 361 RSNPAKIVPAKSKNK 375
Db 360 RSSSARAARNRVKXE 374

RESULT 10
AAE15288
ID AAE15288 standard; protein; 374 AA.
XX
AC AAE15288;
XX
DT 07-MAR-2002 (first entry)
XX
DE Maize LPAAT protein.
XX
KW Lysophosphatidic acid acyltransferase; LPAAT protein; trauma;
KW 1-acyl sn-glycerol-3-phosphate acyltransferase; reoxygenation injury;
KW cellular pathway regulation; trilineage haematopoiesis; inflammation;
KW cytoinductive therapy; adult respiratory distress syndrome; hypoxia;
KW sepsis; maize.
XX
OS Zea mays.
XX
FN US6300487-B1.
XX
PD 09-OCT-2001.
XX
PF 18-DEC-1998; 98US-00215252.
XX
PR 19-MAR-1996; 96US-00618651.
XX
PA (CELL-) CELL THERAPEUTICS INC.
XX
PI Leung DW, Adourel D, Hollenback D;
XX
XX WPI; 2002-033181/04.
XX
PF New nucleic acid encoding human lysophosphatidic acid acyltransferase,
PT useful for identifying specific inhibitors, e.g. for inhibiting
PT inflammation.
XX
PS Disclosure; Fig 2; 69pp; English.
XX
CC The present invention relates to polypeptides with lysophosphatidic acid
CC acyltransferase (LPAAT) activity and polynucleotides encoding such
CC polypeptides. LPAAT also referred as 1-acyl sn-glycerol-3-phosphate
CC acyltransferase (EC 2.3.1.51), catalyses the acylation of
CC lysophosphatidic acid (LPA) to phosphatidic acid (PA). Polypeptides of
CC the invention are used for identifying specific modulators, potentially
CC useful for regulating cellular pathways, e.g. to augment trilineage
CC haematopoiesis after cytoreductive therapy or to inhibit inflammation
CC after hypoxia and reoxygenation injury (e.g. sepsis, trauma and adult
CC respiratory distress syndrome). The present sequence is maize LPAAT
CC protein
XX
SQ Sequence 374 AA;

Query Match 75.0%; Score 1450.5; DB 5; Length 374;
Best Local Similarity 70.7%; Pred. No. 3.1e-143;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

Qy 1 MAIAAAVVLGLLFPAGSLVNLVIAQICVYVVRPVSKSLYRINRVVAELLWLEIWL 60
Db 1 MAIPLVVLVGLLFLLSGLVNAIQAVLVFTIRPFSKSFYRINRFLAELLWLQVWV 60
Qy 61 IDWAGVQVQIETDHTFRLMGKEHALVISNHRSDIDMLVGWVSQRCGCLGSLTAVMKK 120

Db 61 VDWAGVQVQLHAEDETYRSMGKEHALVISNHRSDIDMLGILWILAQRSGLGSLTAVMKK 120
Qy 121 SSKELPVIGWMTSEVILFLERSWAKDESTLKSGIORLSDPFLPFWLALFVEGTRFTQAK 180
Db 121 SSKELPVIGWMTSEVILFLERSWAKDEKTLKWLQRLKDPFRPFWLALFVEGTRFTPAK 180
Qy 181 LLAQAEYATSTGLPVPVRNVLPRTKGFVSVAVSHMRSEFVPAIYDVTVTAIPKSSPAPTMLRL 240
Db 181 LLAQAEYAAASQCLPAPRNVLPRTKGFVSVAVSHMRSEFVPAIYDVTVTVPKDSPOPTMLRI 240
Qy 241 PKQPSVVVHHIKHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300
Db 241 LKQSSVHVHRMKGHAMSEMPKSDSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
Qy 301 RPIKSLVWISWACLWVAGSVKFLQSSLLSSWKGVAFAFGLAVVTALMQILTIQFSQSE 360
Db 300 RPKVSLVTVFWSCLLLFGLAIEFEKWTQLLSTWRGVAFAGMALVTGVHVFIMFSQAE 359
Qy 361 RSNPAKIVPAKSKNK 375
Db 360 RSSSARAARNRVKXE 374

RESULT 11
AAE08477
ID AAE08477 standard; protein; 374 AA.
XX
AC AAE08477;
XX
DT 20-DEC-2000 (first entry)
XX
DE Amino acid sequence of a lysophosphatidic acid acetyltransferase.
XX
KW Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;
KW triacylglycerol; oil content.
XX
OS Oryza sativa.
XX
FN WO200049156-A2.
XX
PD 24-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-US004526.
XX
PR 22-FEB-1999; 99US-0121119P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caboon EB, Caboon RE, Hitz WD, Kinney AJ, Ripp KG;
XX
XX WPI; 2000-588300/51.
XX
DR N-PSDB; AAA64199.
XX
PT New nucleic acid fragment encoding a lysophosphatidic acid
PT acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants
PT which encode LPAAT at higher or lower levels than normal.
XX
PS Claim 31; Page 97-99; 102pp; English.
XX
CC The present sequence represents a lysophosphatidic acid acetyltransferase
CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic
CC plants which encode LPAAT at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found.
CC This would have the effect of altering the level of specific
CC triacylglycerols in those cells, for e.g. overexpression of an LPAAT
CC similar to the maize LPAAT will result in higher oil content in the seed,
CC stem and leaf. LPAAT chimeric genes may be used for co-suppression of
CC genes encoding LPAAT. The polynucleotides may also be used as probes for
CC genetically and physically mapping the genes that are a part of, and as
XX markers for traits linked to those genes
XX
SQ Sequence 374 AA;

Query Match 74.0%; Score 1431.5; DB 3; Length 374;
Best Local Similarity 71.9%; Pred. No. 3.1e-141; Mismatches 55; Indels 1; Gaps 1;
Matches 263; Conservative 47

CC This would have the effect of altering the level of specific
CC triacylglycerols in those cells, for e.g. overexpression of an LPAAT
CC similar to the maize LPAAT will result in higher oil content in the seed,
CC stem and leaf. LPAAT chimeric genes may be used for co-suppression of
CC genes encoding LPAAT. The polynucleotides may also be used as probes for
CC genetically and physically mapping the genes that are a part of, and as
CC markers for traits linked to those genes
XX

QY 1 MAIAAAVVPVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLMLELVL 60
DB 1 MAVPLVLVLPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLMLELVL 60

QY 61 IDWAGVKVQIETDHTFRLMGKEHALVISNHRSDIDWLVGVSAQSGCLGSLTAVMKK 120
DB 61 VDWAGVKVQLHADDETYKAMGNEHALVISNHRSDIDWLVGVSAQSGCLGSLTAVMKK 120

QY 121 SSKFLPVIGSMWFMFSEYLFERSWAKDETLKSGIQRLSDFFLPFWLALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWFAEYLFERSWAKDETLKWLQQLKDFRPFWALFVEGTRFTPAK 180

QY 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIKSSPATMLRL 240
DB 181 LLAQAEYAVSQGLPAPRNVLIPRTKGFVSAVTIMRDFVPAIYDVTIIPKDSFQPTMLRI 240

QY 241 FKQPSVHVHVKHLMKELPDTDEAVAQCRDIFVAKDALLDKHMAEGTFSDQLQDTG 300
DB 241 LKQSSVHVHVKHLMKELPDTDEAVAQCRDIFVAKDALLDKHMAEGTFSDQLQDTG 300

QY 301 RPIKSLVIVISWACLIVVAGSVKFLQWSLLSSWKGVAFSAFGLAVVTALMQILIOFSQSE 360
DB 300 RPKVSLVIVISWACLIVVAGSVKFLQWSLLSSWKGVAFSAFGLAVVTALMQILIOFSQSE 360

QY 361 RSNPAK 366
DB 360 RSSSAK 365

RESULT 12
AAB08479
ID AAB08479 standard; protein; 374 AA.
AC AAB08479;
XX
XX
XX 20-DEC-2000 (first entry)
XX
XX Amino acid sequence of a lysophosphatidic acid acetyltransferase.
XX
XX Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;
XX triacylglycerol; oil content.
XX
XX Triticum aestivum.
XX
XX W0200049156-A2.
XX
XX 24-AUG-2000.
XX
XX 22-FEB-2000; 2000WO-US004526.
XX
XX 22-FEB-1999; 99US-0121119P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;
XX
XX WPI; 2000-558300/51.
XX
XX N-ESDB; AAA64201.
XX
XX New nucleic acid fragment encoding a lysophosphatidic acid
XX acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants
XX which encode LPAAT at higher or lower levels than normal.
XX
XX Claim 31; Page 101-102; 102pp; English.
XX
XX The present sequence represents a lysophosphatidic acid acetyltransferase
XX (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic
XX plants which encode LPAAT at higher or lower levels than normal or in
XX cell types or developmental stages in which they are not normally found.
XX

QY 1 MAIAAAVVPVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLMLELVL 60
DB 1 MAVPLVLVLPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLMLELVL 60

QY 61 IDWAGVKVQIETDHTFRLMGKEHALVISNHRSDIDWLVGVSAQSGCLGSLTAVMKK 120
DB 61 VDWAGVKVQLHADDETYKAMGNEHALVISNHRSDIDWLVGVSAQSGCLGSLTAVMKK 120

QY 121 SSKFLPVIGSMWFMFSEYLFERSWAKDETLKSGIQRLSDFFLPFWLALFVEGTRFTQAK 180
DB 121 SSKFLPVIGSMWFAEYLFERSWAKDETLKWLQQLKDFRPFWALFVEGTRFTPAK 180

QY 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIKSSPATMLRL 240
DB 181 LLAQAEYAVSQGLPAPRNVLIPRTKGFVSAVTIMRDFVPAIYDVTIIPKDSFQPTMLRI 240

QY 241 FKQPSVHVHVKHLMKELPDTDEAVAQCRDIFVAKDALLDKHMAEGTFSDQLQDTG 300
DB 241 LKQSSVHVHVKHLMKELPDTDEAVAQCRDIFVAKDALLDKHMAEGTFSDQLQDTG 300

QY 301 RPIKSLVIVISWACLIVVAGSVKFLQWSLLSSWKGVAFSAFGLAVVTALMQILIOFSQSE 360
DB 300 RPKVSLVIVISWACLIVVAGSVKFLQWSLLSSWKGVAFSAFGLAVVTALMQILIOFSQSE 360

QY 361 RSNPAK 366
DB 360 RSSSAK 365

RESULT 13
AAG31583
ID AAG31583 standard; protein; 376 AA.
AC AAG31583;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 37953.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; Genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EF1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX
XX 05-MAR-1999; 99US-0123180P.
XX
XX 09-MAR-1999; 99US-0123548P.
XX
XX 23-MAR-1999; 99US-0125788P.
XX
XX 25-MAR-1999; 99US-0126264P.
XX
XX 29-MAR-1999; 99US-0126785P.
XX
XX 01-APR-1999; 99US-0127462P.
XX
XX 06-APR-1999; 99US-0128234P.
XX

PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 98US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135112P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137598P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139763P.
PR 22-JUN-1999; 99US-0139817P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144326P.
PR 19-JUL-1999; 99US-0144327P.
PR 19-JUL-1999; 99US-0144328P.
PR 19-JUL-1999; 99US-0144329P.
PR 19-JUL-1999; 99US-0144330P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145066P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
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DB 61 ERWAKDESLKSGIORLSDFPLFWLALFVEGTRFTQAKLLAAQEVATSTGLVPVRNV 120
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DB 181 PESDQIAQWCRDQFVAKDALLDKHIAADTFPGQEQNIGRPKSLAVIWSACLVTLGA 240
QY 321 VKFLQWSSLSSKWKGVAFSAFGLAVVTALMQILIQFSQSERSNPAPKVPKSKN 374
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RESULT 15
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